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(54) Title: ACQUIRED RESISTANCE NPR GENES AND USES THEREOF

(57) Abstract

Genomic and cDNA sequences encoding plant acquired resistance proteins are disclosed. Expression of these polypeptides in transgenic plants are useful for providing enhanced defense mechanisms to combat plant diseases.

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## ACQUIRED RESISTANCE NPR GENES AND USES THEREOF

Background of the Invention

5 This invention relates to the fields of genetic engineering, plant biology, plant pathogen defense genes and their proteins, and crop protection.

Recent advances in plant pathology have provided a basis for understanding the cellular and molecular genetic mechanisms by which plants defend themselves against pathogen attack. In particular, plants are known to utilize at least two different types of defense mechanisms: (i) the hypersensitive response ("HR") and (ii) acquired resistance ("AR"), including systemic acquired resistance ("SAR") and local acquired resistance ("LAR"). These defense mechanisms are discussed below.

The Hypersensitive Response

Plants respond in a variety of ways to pathogenic microorganisms (Lamb, *Cell* 76:419-422, 1994; Lamb et al., *Cell* 56:215-224, 1989). One well-studied defense response that occurs at the site of infection is called the hypersensitive response ("HR") and involves rapid localized necrosis of the infected plant cells or tissue or both. The rapid death of the infected cells is thought to deprive invading pathogens of a sufficient nutrient supply, arresting pathogen growth. Cells undergoing a HR exhibit nuclear DNA fragmentation (for example, DNA laddering), a hallmark of apoptosis first described in animal systems, indicating that the HR involves active, programmed cell death (Mittler et al., *Plant Physiol.* 108:489-493, 1995; Greenberg et al., *Cell* 77: 551-563, 1994; Ryerson and Heath, *Plant Cell* 8:393-402, 1996; Wang et al., *Plant Cell* 8, 375-391, 1996). The HR is also accompanied by a membrane-associated oxidative burst that results in the NADPH-dependent production of  $O_2^-$  and  $H_2O_2$ . These reactive oxygen species may be directly toxic to invading pathogens or may be involved in the crosslinking of plant cell walls surrounding the lesion to form a barrier to infection (Bradley et al., *Cell* 70:21-30, 1992; Levine et al., *Cell* 79:583-593, 1994).

In the 1950s, H.H. Flor developed a well-known genetic model that explains the observation that some races (strains) of a particular pathogen elicited a strong HR on a given cultivar of a host species, whereas other races (strains) of the same pathogen proliferated and caused disease (Flor, *Annu. Rev. Phytopathol.* 9:275-296, 1971). A pathogen that elicits an HR is said to be **avirulent** on that host, the host is said to be **resistant**, and the

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plant-pathogen interaction is said to be **incompatible**. In contrast, strains which cause disease on a particular host are said to be **virulent**, the host is said to be **susceptible**, and the plant-pathogen interaction is said to be **compatible**. In many cases, the molecular basis of incompatibility appears to be due to a gene-for-gene correspondence between pathogen

5 "avrulence" (*avr*) genes and host "resistance" (*R*) genes (Flor, *Annu. Rev. Phytopathol.* 9:275-296, 1971). A plant carrying a particular resistance gene will be resistant to pathogens carrying the corresponding *avr* gene. A simple molecular explanation for this gene-for-gene correspondence between *avr* and *R* genes is that *avr* genes generate signals for which resistance genes encode the cognate receptors. A signal transduction pathway then carries the

10 *avr*-generated signal to a set of target genes which initiates the HR and other host defenses (Gabriel and Rolfe, *Annu. Rev. Phytopathol.* 28:365-391, 1990; Keen, *Plant Mol. Biol.* 19:109-122, 1992; Lamb et al., *Cell* 56:215-224, 1989).

A variety of *avr* genes have been cloned from bacterial and fungal phytopathogens (Keen, *Plant Mol. Biol.* 19:109-122, 1992) and, in at least two cases, gene-for-gene

15 interactions have been demonstrated by experiments showing that a purified *avr*-generated signal molecule will elicit an HR (Culver and Dawson, *Mol. Plant-Microbe Interact.* 4:458-463, 1991; Joosten et al., *Nature* 367:384-386, 1994; Knorr and Dawson, *Proc. Natl. Acad. Sci., USA* 85:170-174, 1988; van den Ackerveken et al., *Plant J.* 7:359-366, 1992). Several plant resistance genes have also been cloned in the past four years that conform to a

20 classic gene-for-gene relationship. These include the tomato *PTO* gene (resistance to strains of *P. syringae* pv *tomato* expressing the avirulence gene *avrPto* (Martin et al., *Science* 262:1432-1436, 1993)), the *Arabidopsis* *RPS2* and *RPM1* genes (resistance to *P. syringae* expressing the avirulence genes *avrRpt2* or *avrRpm1*, respectively (Bent et al., *Science* 265:1856-1860, 1994; Grant et al., *Science* 269:843-846 1995; Mindrinos et al., *Cell*

25 78:1089-1099, 1994)), the tobacco *N* gene (resistance to tobacco mosaic virus (Whitham et al., *Cell* 78:1101-1105, 1994)), the tomato *Cf9* and *Cf2* genes (resistance to the fungal pathogen *C. fulvum* (Dixon et al., *Cell* 84:451-459, 1996; Jones et al., *Science* 266, 789-794, 1994)), the flax *L<sub>6</sub>* gene (resistance to the fungal pathogen *Melampsora lini* (Lawrence et al., *Plant Cell* 7:1195-1206, 1995)), and the rice *Xa21* gene (resistance to *Xanthomonas oryzae*

30 (Song et al., *Science* 270:1804-1806, 1995)).

Acquired Resistance--Systemic and Local Acquired Resistance

The HR not only blocks the local growth of an infecting pathogen, it is also thought to trigger additional defense responses in uninfected parts of the plant which become resistant to a variety of normally virulent pathogens (Enyedi et al., *Cell* 70:879-886, 1992; Malamy and Klessig, *Plant J.* 2:643-654, 1992). This latter phenomenon is called systemic acquired resistance (SAR) and is thought to be the consequence of the concerted activation of many genes that are often referred to as pathogenesis-related ("PR") genes. The biological functions of many of these PR genes remain unknown; however, a large body of physiological, biochemical, and molecular evidence suggests that particular PR genes play a direct role in conferring resistance to pathogens. For example, some PR genes encode chitinases and  $\beta$ -1,3-glucanases which directly inhibit pathogen growth *in vitro* (Mauch et al., *Plant Physiol.* 88:936-942, 1988; Ponstein et al., *Plant Physiol.* 104:109-118, 1994; Schlumbaum et al., *Nature* 324:365-367, 1986; Sela-Buurlage et al., *Plant Physiol.* 101:857-863, 1993; Terras et al., *J. Biol. Chem.* 267:15301-15309, 1992; Woloshuk et al., *Plant Cell* 3:619-628, 1991). In addition, constitutive expression in transgenic plants of PR genes has been shown to decrease disease susceptibility in a limited number of cases (Alexander et al., *Proc Natl. Acad. Sci. USA* 90:7327-7331, 1993; Liu et al., *Proc. Natl. Acad. Sci. USA* 91:1888-1892, 1994; Terras et al., *Plant Cell* 7:573-588, 1995; Zhu et al., *Bio/Technology* 12:807-812, 1994).

SAR was originally defined by Ross (*Virology* 14:340-358, 1961), who demonstrated that tobacco became resistant to infection by a number of viruses after a primary inoculation with an avirulent strain of tobacco mosaic virus. Subsequently, it was demonstrated that SAR could also be elicited by other viruses, bacteria, and fungi, and that the resistance induced by any particular pathogen was effective against a broad spectrum of viral, bacterial, and fungal diseases (Cameron et al., *Plant J.* 5:715-725, 1994; Cruikshank and Mandryk, *J. Aust. Inst. Agric. Sci.* 26:369-372, 1960; Dempsey et al., *Phytopathology* 83:1021-1029, 1993; Hecht and Bateman, *Phytopathology* 54:523-530, 1964; Kuc, *BioScience* 39:854-860, 1982; Lovrekovich et al., *Phytopathology* 58:1034-1035, 1968; Mauch-Mani and Slusarenko, *Mol. Plant-Microbe Interact.* 7:378-383, 1994; Uknes et al., *Mol. Plant-Microbe Interact.* 6:692-698, 1993).

Another acquired plant defense response that shares many features with SAR is

so-called local acquired resistance or "LAR." LAR develops in the direct vicinity of a successfully proliferating pathogen to block further spread of the pathogen and to thwart the occurrence of secondary infections. The same set of PR proteins is believed to be involved in conferring resistance by both LAR and SAR, and, as described below, the same signalling molecules also appear to be required for the onset of both responses.

Certain chemicals, such as salicylic acid (SA), 2,6-dichloroisonicotinic acid (INA), and benzo(1,2,3)thiadiazole-7-carbothioic acid S-methyl ester (BTH) have been shown to induce SAR or LAR or both when applied exogenously to plants (White, *Virology* 99:410-412, 1979; Metraux et al., *Science* 250:1004-1006, 1991; Görlach et al., *Plant Cell* 8:629-643, 1996). Moreover, several lines of evidence indicate that endogenously produced SA is involved in the signal transduction pathway(s) coupling HR with the onset of SAR. In tobacco and cucumber, an increase in SA concentration has been observed after an avirulent pathogen infection when accompanied by the establishment of SAR (Goodman and Plurad, *Physiol. Plant. Pathol.* 1:11-16, 1971; Malamy et al., *Science* 250:1002-1004, 1990; Metraux et al., *Science* 250:1004-1006, 1990; Rasmussen et al., *Plant Physiol.* 97:1342-1347, 1991). The accumulation of SA is also associated with the subsequent induction of genes including those encoding PR proteins (Van Loon and Van Kammen, *Virology* 40:199-211, 1970; Ward et al., *Plant Cell* 3:1085-1094, 1991; Yalpani et al., *Plant Cell* 3:809-818, 1991). In tobacco and *Arabidopsis*, exogenously applied SA can induce the accumulation of PR mRNAs, which is a characteristic of SAR (Uknes et al., *Plant Cell* 4:645-656, 1992; Ward et al., *Plant Cell* 3:1085-1094, 1991; White, *Virology* 99:410-412, 1979).

These results have led to the hypothesis that one of the consequences of pathogen infection is the accumulation of SA *in vivo*, which induces the expression of a set of proteins that act to limit further infection of the host (Ward et al., *Plant Cell* 3:1085-1094, 1991).

Direct support for this hypothesis has come from the observation that transgenic tobacco or *Arabidopsis* plants that express a bacterial gene encoding a salicylate hydroxylase are unable to accumulate SA and, consequently, do not exhibit either SAR or LAR (Gaffney et al., *Science* 261:754-756, 1993). Thus, SA is thought to be required *in vivo* for the establishment of SAR and LAR, and, as described above, PR gene products appear to participate directly in conferring pathogen resistance.

### Summary of the Invention

In general, the invention features an isolated nucleic acid molecule including a sequence encoding an acquired resistance (AR) polypeptide, wherein the acquired resistance polypeptide is at least 40% (and preferably 50%, 70%, 80%, or 90%) identical to the amino acid sequence of Fig. 5 (SEQ ID NO:3) or Fig. 7B (SEQ ID NO:14). Preferably, such a nucleic acid molecule encodes an acquired resistance polypeptide that mediates the expression of a pathogenesis-related polypeptide. In another preferred embodiment, the acquired resistance polypeptide includes an ankyrin-repeat motif.

Nucleic acid molecules of the invention are derived from any plant species, including, without limitation, angiosperms (for example, dicots and monocots) and gymnosperms. Exemplary plants from which the nucleic acid may be derived include, without limitation, sugar cane, wheat, rice, maize, sugar beet, potato, barley, manioc, sweet potato, soybean, sorghum, cassava, banana, grape, oats, tomato, millet, coconut, orange, rye, cabbage, apple, watermelon, canola, cotton, carrot, garlic, onion, pepper, strawberry, yam, peanut, onion, bean, pea, mango, and sunflower. Preferred nucleic acid molecules are derived from cruciferous plants, for example, *Arabidopsis thaliana*. Examples of cruciferous acquired resistance molecules are shown in Fig. 4 (NPR genomic DNA; SEQ ID NO:1) and Fig. 5 (NPR cDNA; SEQ ID NO:2). Other preferred nucleic acid molecules are derived from solanaceous plants, for example, *Nicotiana glutinosa*. An example of such a solanaceous acquired resistance molecule is shown in Fig. 7A (SEQ. ID NO:13).

In another aspect, the invention features an isolated nucleic acid molecule (for example, a DNA molecule) that encodes an acquired resistance polypeptide that specifically hybridizes to a nucleic acid molecule that includes the nucleic acid sequence of Fig. 4 (NPR genomic DNA; SEQ ID NO:1), Fig. 5 (NPR cDNA; SEQ ID NO:2), or Fig. 7A (SEQ ID NO:13). Preferably, the specifically hybridizing nucleic acid molecule encodes an acquired resistance polypeptide that mediates the expression of a pathogenesis-related polypeptide. In another preferred embodiment, the specifically hybridizing nucleic acid molecule encodes an acquired resistance polypeptide including an ankyrin-repeat motif. In yet other preferred embodiments, the specifically hybridizing nucleic acid molecule complements an acquired resistance mutant (for example, an *Arabidopsis npr* mutant). The invention also features an RNA transcript having a sequence complementary to any of the isolated nucleic acid

molecules described above.

In related aspects, the invention further features a cell or a vector (for example, a plant expression vector), each of which includes an isolated nucleic acid molecule of the invention. In preferred embodiments, the cell is a bacterium (for example, *E. coli* or *Agrobacterium tumefaciens*) or is a plant cell (for example, is a cell from any of the crops listed above).  
5 Such a plant cell has an increased level of resistance against a disease caused by a plant pathogen (for example, *Phytophthora*, *Peronospora*, or *Pseudomonas*). In yet another preferred embodiment, the isolated nucleic acid molecule of the invention is operably linked to an expression control region that mediates expression of a polypeptide encoded by the  
10 nucleic acid molecule. For example, the expression control region is capable of mediating constitutive, inducible (for example, pathogen- or wound-inducible), or cell- or tissue-specific gene expression. The invention further features a cell (for example, a bacterium such as *E. coli* or *Agrobacterium tumefaciens*, or a plant cell) which contains the vector of the invention.

In still another aspect, the invention features a transgenic plant including any of the  
15 above nucleic acid molecules of the invention integrated into the genome of the plant, wherein the nucleic acid molecule is expressed in the transgenic plant. In addition, the invention features seeds and cells from such transgenic plants. For example, such transgenic plants may be produced according to conventional methods using any of the above crop plants.

In yet another aspect, the invention features a substantially pure acquired resistance  
20 polypeptide including an amino acid sequence that has at least 40% (and preferably, 50%, 60%, 70%, 80% or 90%) identity to the amino acid sequence of Fig. 5 (SEQ ID NO:3) or Fig. 7B (SEQ ID NO:14). Preferably, the acquired resistance polypeptide mediates the expression of a pathogenesis-related polypeptide. In other preferred  
25 embodiments, the acquired resistance polypeptide includes an ankyrin-repeat motif or a G-protein coupled receptor motif. Such acquired resistance polypeptides are derived from any plant species, for example, those crop plants mentioned above. In preferred embodiments, the polypeptide of the invention is derived from a cruciferous species, for example, *Arabidopsis thaliana*, or from a solanaceous species, for example, *Nicotiana glutinosa*.

30 In a related aspect, the invention also features a method of producing an acquired resistance polypeptide. The method involves: (a) providing a cell transformed with a nucleic



acid molecule of the invention positioned for expression in the cell; (b) culturing the transformed cell under conditions for expressing the nucleic acid molecule; and (c) recovering the acquired resistance polypeptide. The invention further features a recombinant acquired resistance polypeptide produced by such expression of an isolated nucleic acid molecule of the invention, and a substantially pure antibody that specifically recognizes and binds to an acquired resistance polypeptide or a portion thereof.

In another aspect, the invention features a method of providing an increased level of resistance against a disease caused by a plant pathogen in a transgenic plant. The method involves: (a) producing a transgenic plant cell including the nucleic acid molecule of the invention integrated into the genome of the transgenic plant cell and positioned for expression in the plant cell; and (b) growing a transgenic plant from the plant cell wherein the nucleic acid molecule is expressed in the transgenic plant and the transgenic plant is thereby provided with an increased level of resistance against a disease caused by a plant pathogen.

In another aspect, the invention features methods of isolating an acquired resistance gene or fragment thereof. The first method involves: (a) contacting the nucleic acid molecule of the invention or a portion thereof with a preparation of DNA from a plant cell under hybridization conditions providing detection of DNA sequences having 40% or greater sequence identity to the nucleic acid sequence of Fig. 4 (SEQ ID NO:1), Fig. 5 (SEQ ID NO:2), or Fig. 7A (SEQ ID NO:13); and (b) isolating the hybridizing DNA as an acquired resistance gene or fragment thereof. The second method involves: (a) providing a sample of plant cell DNA; (b) providing a pair of oligonucleotides having sequence homology to a region of a nucleic acid molecule of the invention; (c) contacting the pair of oligonucleotides with the plant cell DNA under conditions suitable for polymerase chain reaction-mediated DNA amplification; and (d) isolating the amplified acquired resistance gene or fragment thereof.

In preferred embodiments of the second method, the amplification step is carried out using a sample of cDNA prepared from a plant cell. In addition, the pair of oligonucleotides used in the second method are based on a sequence encoding an acquired resistance polypeptide, wherein the acquired resistance polypeptide is at least 40% (and preferably 50%, 60%, 70%, 80%, or 90%) identical to the amino acid sequence of Fig. 5 (SEQ ID NO:3) or Fig. 7B (SEQ ID NO:14).

By "acquired resistance" gene or "AR" gene is meant a gene encoding a polypeptide capable of triggering a plant acquired resistance response (for example, a systemic acquired resistance (SAR) or local acquired resistance response (LAR)) in a plant cell or plant tissue. This response may occur at the transcriptional level or it may be enzymatic or structural in nature. AR genes may be identified and isolated from any plant species, especially agronomically important crop plants, using any of the sequences disclosed herein in combination with conventional methods known in the art.

By "polypeptide" is meant any chain of amino acids, regardless of length or post-translational modification (for example, glycosylation or phosphorylation).

By "pathogenesis-related" polypeptide or "PR" polypeptide is meant a polypeptide that is expressed in conjunction with the establishment of SAR or LAR. Exemplary PR proteins include, without limitation, chitinase, PR-1a, PR1, PR5, GST (glutathione-S-transferase), and  $\beta$ -1,3 glucanase, osmotin, thionin, glycine-rich proteins (GRPs), phenylalanine ammonia lyase (PAL), and lipoxygenase (LOX).

By "ankyrin-repeat" motif is meant a consensus motif that is found in a wide variety of proteins that are capable of mediating protein-protein interactions. Ankyrin-repeat motifs are described in Michaely and Bennett (*Trends in Cell Biology* 2:127-129, 1992) and Bork (*Proteins: Structure, Function, and Genetics* 17:363-374, 1993).

By "substantially identical" is meant a polypeptide or nucleic acid exhibiting at least 40%, preferably 50%, more preferably 80%, and most preferably 90%, or even 95% homology to a reference amino acid sequence (for example, the amino acid sequence shown in Fig. 5 (SEQ ID NO:3) or Fig. 7B (SEQ ID NO:14)) or nucleic acid sequence (for example, the nucleic acid sequences shown in Fig. 4, or Fig. 5, or Fig. 7A, SEQ ID NOS:1, 2, and 13, respectively). For polypeptides, the length of comparison sequences will generally be at least 16 amino acids, preferably at least 20 amino acids, more preferably at least 25 amino acids, and most preferably 35 amino acids. For nucleic acids, the length of comparison sequences will generally be at least 50 nucleotides, preferably at least 60 nucleotides, more preferably at least 75 nucleotides, and most preferably 110 nucleotides.

Sequence identity is typically measured using sequence analysis software (for example, Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705, BLAST,

or PILEUP/PRETTYBOX programs). Such software matches identical or similar sequences by assigning degrees of homology to various substitutions, deletions, and/or other modifications. Conservative substitutions typically include substitutions within the following groups: glycine alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid, asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine.

By a "substantially pure polypeptide" is meant an AR polypeptide (for example, an NPR polypeptide such as NPR1) that has been separated from components which naturally accompany it. Typically, the polypeptide is substantially pure when it is at least 60%, by weight, free from the proteins and naturally-occurring organic molecules with which it is naturally associated. Preferably, the preparation is at least 75%, more preferably at least 90%, and most preferably at least 99%, by weight, an AR polypeptide. A substantially pure AR polypeptide may be obtained, for example, by extraction from a natural source (for example, a plant cell); by expression of a recombinant nucleic acid encoding an AR polypeptide; or by chemically synthesizing the protein. Purity can be measured by any appropriate method, for example, column chromatography, polyacrylamide gel electrophoresis, or by HPLC analysis.

By "derived from" is meant isolated from or having the sequence of a naturally-occurring sequence (e.g., a cDNA, genomic DNA, synthetic, or combination thereof).

By "isolated DNA" is meant DNA that is free of the genes which, in the naturally-occurring genome of the organism from which the DNA of the invention is derived, flank the gene. The term therefore includes, for example, a recombinant DNA that is incorporated into a vector; into an autonomously replicating plasmid or virus; or into the genomic DNA of a prokaryote or eukaryote; or that exists as a separate molecule (for example, a cDNA or a genomic or cDNA fragment produced by PCR or restriction endonuclease digestion) independent of other sequences. It also includes a recombinant DNA which is part of a hybrid gene encoding additional polypeptide sequence.

By "specifically hybridizes" is meant that a nucleic acid sequence is capable of hybridizing to a DNA sequence at least under low stringency conditions as described herein, and preferably under high stringency conditions, also as described herein.

By "transformed cell" is meant a cell into which (or into an ancestor of which) has been introduced, by means of recombinant DNA techniques, a DNA molecule encoding (as

used herein) an AR polypeptide.

By "positioned for expression" is meant that the DNA molecule is positioned adjacent to a DNA sequence which directs transcription and translation of the sequence (i.e., facilitates the production of, for example, an AR polypeptide, a recombinant protein, or an RNA molecule).

By "reporter gene" is meant a gene whose expression may be assayed; such genes include, without limitation,  $\beta$ -glucuronidase (GUS), luciferase, chloramphenicol transacetylase (CAT), green fluorescent protein (GFP),  $\beta$ -galactosidase, herbicide resistant genes and antibiotic resistance genes.

By "expression control region" is meant any minimal sequence sufficient to direct transcription. Included in the invention are promoter elements that are sufficient to render promoter-dependent gene expression controllable for cell-, tissue-, or organ-specific gene expression, or elements that are inducible by external signals or agents (for example, light-, pathogen-, wound-, stress-, or hormone-inducible elements or chemical inducers such as SA or INA); such elements may be located in the 5' or 3' regions of the native gene or engineered into a transgene construct.

By "operably linked" is meant that a gene and a regulatory sequence(s) are connected in such a way as to permit gene expression when the appropriate molecules (for example, transcriptional activator proteins) are bound to the regulatory sequence(s).

By "plant cell" is meant any self-propagating cell bounded by a semi-permeable membrane and containing a plastid. Such a cell also requires a cell wall if further propagation is desired. Plant cell, as used herein includes, without limitation, algae, cyanobacteria, seeds, suspension cultures, embryos, meristematic regions, callus tissue, leaves, roots, shoots, gametophytes, sporophytes, pollen, and microspores.

By "crucifer" is meant any plant that is classified within the Cruciferae family. The Cruciferae include many agricultural crops, including, without limitation, rape (for example, *Brassica campestris* and *Brassica napus*), broccoli, cabbage, brussel sprouts, radish, kale, Chinese kale, kohlrabi, cauliflower, turnip, rutabaga, mustard, horseradish, and *Arabidopsis*.

By "transgene" is meant any piece of DNA which is inserted by artifice into a cell, and becomes part of the genome of the organism which develops from that cell. Such a transgene may include a gene which is partly or entirely heterologous (i.e., foreign) to the

transgenic organism, or may represent a gene homologous to an endogenous gene of the organism.

By "transgenic" is meant any cell which includes a DNA sequence which is inserted by artifice into a cell and becomes part of the genome of the organism which develops from that cell. As used herein, the transgenic organisms are generally transgenic plants and the DNA (transgene) is inserted by artifice into the nuclear or plastidic genome. A transgenic plant according to the invention may contain one or more acquired resistance genes.

By "pathogen" is meant an organism whose infection of viable plant tissue elicits a disease response in the plant tissue. Such pathogens include, without limitation, bacteria, mycoplasmas, fungi, insects, nematodes, viruses, and viroids. Plant diseases caused by these pathogens are described in Chapters 11-16 of Agrios, *Plant Pathology*, 3rd ed., Academic Press, Inc., New York, 1988.

Examples of bacterial pathogens include, without limitation, *Erwinia* (for example, *E. carotovora*), *Pseudomonas* (for example, *P. syringae*), and *Xanthomonas* (for example, *X. campepestris* and *X. oryzae*).

Examples of fungal disease-causing pathogens include, without limitation, *Alternaria* (for example, *A. brassicola* and *A. solani*), *Ascochyta* (for example, *A. pisi*), *Botrytis* (for example, *B. cinerea*), *Cercospora* (for example, *C. kikuchii* and *C. zaea-maydis*), *Colletotrichum* sp. (for example, *C. lindemuthianum*), *Diplodia* (for example, *D. maydis*), *Erysiphe* (for example, *E. graminis* f.sp. *graminis* and *E. graminis* f.sp. *hordei*), *Fusarium* (for example, *F. nivale* and *F. oxysporum*, *F. graminearum*, *F. solani*, *F. moniliforme*, and *F. roseum*), *Gaeumanomyces* (for example, *G. graminis* f.sp. *tritici*), *Helminthosporium* (for example, *H. turcicum*, *H. carbonum*, and *H. maydis*), *Macrophomina* (for example, *M. phaseolina* and *Maganaporthe grisea*), *Nectria* (for example, *N. heamatocacca*), *Peronospora* (for example, *P. manshurica*, *P. tabacina*), *Phoma* (for example, *P. betae*), *Phymatotrichum* (for example, *P. omnivorum*), *Phytophthora* (for example, *P. cinnamomi*, *P. cactorum*, *P. phaseoli*, *P. parasitica*, *P. citrophthora*, *P. megasperma* f.sp. *sojae*, and *P. infestans*), *Plasmopara* (for example, *P. viticola*), *Podosphaera* (for example, *P. leucotricha*), *Puccinia* (for example, *P. sorghi*, *P. striiformis*, *P. graminis* f.sp. *tritici*, *P. asparagi*, *P. recondita*, and *P. arachidis*), *Puthium* (for example, *P. aphanidermatum*), *Pyrenophora* (for example, *P. tritici-repentens*), *Pyricularia* (for example, *P. oryzae*), *Pythium* (for example, *P.*

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ultimum), *Rhizoctonia* (for example, *R. solani* and *R. cerealis*), *Scerotium* (for example, *S. rolfsii*), *Sclerotinia* (for example, *S. sclerotiorum*), *Septoria* (for example, *S. lycopersici*, *S. glycines*, *S. nodorum* and *S. tritici*), *Thielaviopsis* (for example, *T. basicola*), *Uncinula* (for example, *U. necator*), *Venturia* (for example, *V. inaequalis*), *Verticillium* (for example, *V. dahliae* and *V. albo-atrum*).

Examples of pathogenic nematodes include, without limitation, root-knot nematodes<sup>1</sup> (for example, *Meloidogyne* sp. such as *M. incognita*, *M. arenaria*, *M. chitwoodi*, *M. hapla*, *M. javanica*, *M. graminicola*, *M. microtyla*, *M. graminis*, and *M. naasi*), cyst nematodes (for example, *Heterodera* sp. such as *H. schachtii*, *H. glycines*, *H. sacchari*, *H. oryzae*, *H. avenae*,  
 10 *H. cajani*, *H. elachista*, *H. goettingiana*, *H. graminis*, *H. mediterranea*, *H. moths*, *H. sorghi*, and *H. zae*, or, for example, *Globodera* sp. such as *G. rostochiensis* and *G. pallida*), root-attacking nematodes (for example, *Rotylenchulus reniformis*, *Tylenchulus semipenetrans*, *Pratylenchus brachyurus*, *Radopholus citrophilus*, *Radopholus similis*, *Xiphinema americanum*, *Xiphinema rivesi*, *Paratrichodorus minor*, *Heterorhabditis heliothidis*, and  
 15 *Bursaphelenchus xylophilus*), and above-ground nematodes (for example, *Anguina funesta*, *Anguina tritici*, *Ditylenchus dipsaci*, *Ditylenchus myceliphagus*, and *Aphenlenchoides besseyi*).

Examples of viral pathogens include, without limitation, tobacco mosaic virus, tobacco necrosis virus, potato leaf roll virus, potato virus X, potato virus Y, tomato spotted  
 20 wilt virus, and tomato ring spot virus.

By "increased level of resistance" is meant a greater level of resistance to a disease-causing pathogen in a transgenic plant (or cell or seed thereof) of the invention than the level of resistance relative to a control plant (for example, a non-transgenic plant). In preferred  
 25 embodiments, the level of resistance in a transgenic plant of the invention is at least 20% (and preferably 30% or 40%) greater than the resistance of a control plant. In other preferred embodiments, the level of resistance to a disease-causing pathogen is 50% greater, 60% greater, and more preferably even 75% or 90% greater than a control plant; with up to 100% above the level of resistance as compared to a control plant being most preferred. The level of resistance is measured using conventional methods. For example, the level of resistance to  
 30 a pathogen may be determined by comparing physical features and characteristics (for example, plant height and weight, or by comparing disease symptoms, for example, delayed

lesion development, reduced lesion size, leaf wilting and curling, water-soaked spots, and discoloration of cells) of transgenic plants.

By "detectably-labelled" is meant any direct or indirect means for marking and identifying the presence of a molecule, for example, an oligonucleotide probe or primer, a gene or fragment thereof, or a cDNA molecule or a fragment thereof. Methods for  
5 detectably-labelling a molecule are well known in the art and include, without limitation, radioactive labelling (for example, with an isotope such as  $^{32}\text{P}$  or  $^{35}\text{S}$ ) and nonradioactive labelling (for example, chemiluminescent labelling, for example, fluorescein labelling).

By "purified antibody" is meant antibody which is at least 60%, by weight, free from  
10 proteins and naturally-occurring organic molecules with which it is naturally associated. Preferably, the preparation is at least 75%, more preferably 90%, and most preferably at least 99%, by weight, antibody, for example, an acquired resistance polypeptide-specific antibody. A purified AR antibody may be obtained, for example, by affinity chromatography using a recombinantly-produced acquired resistance polypeptide and standard techniques.

By "specifically binds" is meant an antibody which recognizes and binds an AR  
15 protein but which does not substantially recognize and bind other molecules in a sample, for example, a biological sample, which naturally includes an AR protein such as NPR.

As discussed above, fundamental acquired resistance genes that are responsible for  
20 providing plants with the ability to protect themselves against pathogens have been identified. Accordingly, the invention provides a number of important advances and advantages for the protection of plants against their pathogens. For example, by providing AR genes as described herein that are readily incorporated and expressed in all species of plants, the invention facilitates an effective and economical means for in-plant protection against plant  
25 pathogens. Such protection against pathogens reduces or minimizes the need for traditional chemical practices (for example, application of fungicides, bactericides, nematicides, insecticides, or viricides) that are typically used by farmers for controlling the spread of plant pathogens and providing protection against disease-causing pathogens. In addition, because plants expressing one or more acquired resistance gene(s) described herein are less vulnerable  
30 to pathogens and their diseases, the invention further provides for increased production efficiency, as well as for improvements in quality and yield of crop plants and ornamentals.

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Thus, the invention contributes to the production of high quality and high yield agricultural products: for example, fruits, ornamentals, vegetables, cereals and field crops having reduced spots, blemishes, and blotches that are caused by pathogens; agricultural products with increased shelf-life and reduced handling costs; and high quality and yield crops for agricultural (for example, cereal and field crops), industrial (for example, oilseeds), and commercial (for example, fiber crops) purposes. Furthermore, because the invention reduces the necessity for chemical protection against plant pathogens, the invention benefits the environment where the crops are grown. Genetically-improved seeds and other plant products that are produced using plants expressing the genes described herein also render farming possible in areas previously unsuitable for agricultural production. The invention further provides a means for mediating the expression of pathogenesis-related proteins, for example, chitinase and GST, that confer resistance to plant pathogens. For example, transgenic plants constitutively producing an AR gene product are capable of activating PR gene expression, which in turn confers resistance to plant pathogens. Collective PR gene expression that is mediated by the AR gene product obviates the need to express individual PR genes as a means to promote plant defense mechanisms.

The invention is also useful for providing nucleic acid and amino acid sequences of an AR gene that facilitates the isolation and identification of AR genes from any plant species.

Other features and advantages of the invention will be apparent from the following description of the preferred embodiments thereof, and from the claims.

### Detailed Description

The drawings will first be described.

#### Drawings

Fig. 1 is a schematic illustration showing the physical map of *A. thaliana* chromosome I and the position of *NPR1*.

Fig. 2A is a photograph of a Northern blot analysis showing the expression of the PR-1 gene in wild type plants (Col-0, lanes 1-3), *npr1-2* mutant plants (lanes 4-6), *npr1-2* transformants with a noncomplementing cosmid (m305-2-7, lanes 7-9), and *npr1-2* transformants with complementing cosmids (21A4-P5-1, lanes 10-12 and 21A4-6-1-1, lanes 13-15). RNA samples were prepared from fifteen-day old seedlings grown on MS media



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(lanes 1, 4, 7, 10, and 13), MS media with 0.1 mM INA (lanes 2, 5, 8, 11, and 14), and MS media with 0.1 mM SA (lanes 3, 6, 9, 12, and 15).

Fig. 2B is a series of photographs showing disease symptoms (top panels) and *BGL2-GUS* expression (bottom panels) induced by Psm ES4326 on wild-type (left panels), *npr1-1* (middle panels), and an *npr1-1* transformant with a complementing cosmid (21A4-4-3-1, right panels).

Fig. 2C is a panel of graphs showing the growth of Psm ES4326 in wild-type, *npr1-2*, and an *npr1-2* transformant with a complementing cosmid (21A4-P5-1). Error bars represent 95% confidence limits of log-transformed data as described by Sokal and Rohlf (*Biometry*, 2d ed., W.H. Freeman and Company, New York, 1981).

Fig. 2D is a panel of bar graphs showing the disease rating of *P. parasitica* NOCO infection in wild type, *npr1-2*, and an *npr1-2* transformant with a complementing cosmid (21A4-P5-1). The disease rating scales are defined as follows: 0, no conidiophores on the plant; 1, no more than 5 conidiophores per infected leaf; 2, 3-20 conidiophores on a few infected leaves; 3, 6-20 conidiophores on most infected leaves; 4, 5 or more conidiophores on all infected leaves; 5, 20 or more conidiophores on all infected leaves.

Fig. 3 is a schematic illustration showing the restriction map of the 7.5-kb region containing the *NPR1* gene.

Fig. 4 is a schematic illustration showing the genomic sequence of the 7.5-kb region containing the acquired resistance nucleic acid sequence of the gene termed *NPR1* (SEQ ID NO:1) from *Arabidopsis thaliana*.

Fig. 5 is a schematic illustration showing the cDNA sequence (SEQ ID NO:2) and deduced amino acid sequence (SEQ ID NO:3) of the acquired resistance protein termed NPR1 from *Arabidopsis thaliana*. Amino acids numbered 262-289, 323-371, and 453-469 show homology to a mouse ankyrin protein, an ankyrin-repeat motif, and a G-protein coupled receptor motif, respectively.

Fig. 6A is a schematic illustration showing the alignment of the NPR1 amino acid sequence with mouse ankyrin 3 (ANKB). Two regions producing the highest scoring pairs (smallest sum probability = 0.0004) generated using a BLAST search are shown. The identical and similar amino acids (+) are highlighted in bold, circled letters.

Fig. 6B is a schematic illustration showing the alignment of the ankyrin repeats in

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NPR1 with the ankyrin repeat consensus derived from Michaely and Bennett (Trends in Cell Biology 2:127-129, 1992) and Bork (Proteins: Structure, Function, and Genetics 17:363-374, 1993). Since there are a few non-overlapping amino acids between the two derived consensus sequences, both are presented. In the consensus derived from Bork, the conserved features are indicated: t, turn-like or polar; o, S/T; h, hydrophobic; capitals, conserved amino acids. Those amino acids identical to the consensus are highlighted in bold, circled letters.

Fig. 7A is a schematic illustration showing the cDNA sequence (SEQ ID NO:13) of an NPR1 homolog isolated from *Nicotiana glutinosa*.

Fig. 7B is a schematic illustration showing the deduced amino acid sequence of the NPR1 homolog of *Nicotiana glutinosa* (SEQ ID NO:14) shown in Fig. 7A.

Fig. 8A is a graph illustrating the dosage effect of NPR1 on the resistance of transgenic *Arabidopsis* to the bacterial pathogen, Psm ES4326. Eight samples were taken at each time point for the Psm ES4326 infection (initial inoculant OD<sub>600</sub>=0.001). Error bars represent 95% confidence limits of log-transformed data. Colony forming unit is designated as cfu.

Fig. 8B is a histogram showing the dosage effect of NPR1 on the resistance of transgenic *Arabidopsis* to the fungal pathogen, *Peronospora parasitica* NOCO2. A spore suspension (3x10<sup>4</sup> spores/mL) of *P. parasitica* was used for these infection studies, and the number of conidiophores on each plant was counted seven days after infection. The data were analyzed using Wilcoxon two-sample tests. At the 95% confidence level, significant difference in growth was present between all pairs of samples except ColNPR1-M and ColNPR1-H, and Col and ColNPR1-L.

Fig. 9A are photographs showing the restoration of inducible BGL2-GUS expression in 35S-NPR1-GFP transgenic plants. Seedlings were grown on either MS or MS-INA (0.1 mM) media for fourteen days and stained for GUS activity.

Fig. 9B is a photograph showing the complementation of the SA sensitivity in the *Arabidopsis npr1* mutant by 35S-NPR1-GFP. Seedlings were grown for eleven days on MS-SA (0.5 mM) medium. The NPR1-GFP transgene restored normal growth to *npr1* on SA. The mGFP transgene, however, was unable to restore normal growth to *npr1*. Note that the

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NPR1-GFP line used was in the  $T_2$  generation. The observed 3:1 segregation ratio indicated that the transgenic plants contained a single locus NPR1-GFP insertion.

Fig. 9C is a histogram showing the restoration of *P. parasitica* resistance to the  $T_2$  NPR1-GFP transformants. INA treatment (0.65 mM) was carried out seventy-two hours prior to infection with a spore suspension ( $3 \times 10^4$  spores/mL). The disease symptoms were scored seven days after the infection with respect to the number of conidiophores on the plant. The disease rating scale is defined as: 0, no conidiophores on the plant; 1, no more than 5 conidiophores per infected leaf; 2, 6-20 conidiophores on a few infected leaves; 3, 6-20 conidiophores on most of the infected leaves; 4, 5 or more conidiophores on all infected leaves; 5, 20 or more conidiophores on all infected leaves. Seedlings in the 0, 4, and 5 categories were also examined for the presence of the NPR1-GFP transgene, and the number of NPR1-GFP transformants is indicated in the parenthesis. Most of the *P. parasitica* resistant plants (0 category) contained the NPR1-GFP transgene; however, all of the sensitive plants (4 and 5 categories) were observed to segregate as non-transformants lacking the transgene.

Fig. 10 is a photograph showing the localization of NPR1-GFP in response to chemical activators of SAR. The transformants, containing either the NPR1-GFP (top and bottom panels) or mGFP transgene (middle panels) were grown for eleven days on MS or MS-INA media. GFP fluorescence was visualized by confocal microscopy in leaf mesophyll cells and guard cells. DIC is shown in the red channel and GFP is shown in the green channel.

Figs. 11A-11G are a series of photographs showing the localization of NPR1-GFP in response to Psm ES4326 infection. Leaves of NPR1-GFP transformants were infiltrated on the left half with either Psm ES4326 (Fig. 11B) or 10 mM  $MgCl_2$  (Fig. 11E) and stained for BGL2-GUS expression after three days. Prior to GUS staining the leaves were analyzed for GFP localization on the infiltrated (Fig. 11A and Fig. 11D) and the uninfiltrated (Fig. 11C) side. Leaves of mGFP transformants were infiltrated with Psm ES4326 (Fig. 11F) or 10 mM  $MgCl_2$  (Fig. 11G) and analyzed for GFP localization.

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Overview

A genetic study was conducted using *Arabidopsis thaliana* as a model system to identify key elements that control the signaling pathway leading to the induction of acquired resistance (AR), for example, a system acquired resistance (SAR) response, to pathogen infection in plants. In wild-type *Arabidopsis* plants, SAR responses can be induced by treatment with 0.1 mM salicylic acid (SA) or 0.1 mM 2,6-dichloroisonicotinic acid (INA) or after an infection by an avirulent pathogen such as *Pseudomonas syringae* pv *phaseolicola* NP3121/*avrRpt2* (*P.s. phaseolicola* 3121/*avrRpt2*). SAR is demonstrated by enhanced resistance to virulent pathogens, such as *Pseudomonas syringae* pv *maculicola* ES4326 (*P.s. maculicola* ES4326), and by increased expression of pathogenesis-related genes (for example, *PR* genes including *PR1*, *BGL2*, and *PR5*). To facilitate detection of *PR* gene expression and identification of mutants that were aberrant in the SAR signaling pathway, a *BGL2-GUS* reporter gene was constructed and transformed into *Arabidopsis thaliana* ecotype Columbia. This parental line containing the *BGL2-GUS* transgene was mutagenized by treatment of seeds with 0.3% ethyl methanesulfonate for eleven hours. The M2 progeny of the mutagenized population were screened for the lack of *BGL2-GUS* expression in the presence of the SAR-inducers SA and INA (Cao et al., *Plant Cell* 6:1583-1592, 1994).

Using these techniques, the *npr1-1* (nonexpresser of *PR* genes) mutant was isolated and found to have almost complete lack of expression of the *BGL2-GUS* reporter gene, as well as a lack of expression of the endogenous *PR1*, *BGL2*, and *PR5* genes in response to SA, INA, and avirulent pathogen treatments (Cao et al., *Plant Cell* 6:1583-1592, 1994). Further characterization of the *npr1-1* mutant showed that mutations in the *NPR1* gene completely blocked the induction of SAR. In the *npr1-1* plants pretreated with SA, INA, or an avirulent pathogen, growth of virulent pathogens (for example, *P.s. maculicola* ES4326) was not inhibited, as found in the parental line carrying the wild-type *NPR1* gene. This finding demonstrated that the *NPR1* gene plays a key role in the signaling pathway leading to the establishment of SAR.

Two additional *npr1* mutants, *npr1-2* and *npr1-3*, were isolated on the basis that they were more susceptible to infection than wild-type plants by *P.s. maculicola* strain ES4326

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(Glazebrook et al., *Genetics* 143:973-982, 1996). Genetic complementation tests showed that *npr1-1*, *npr1-2*, and *npr1-3* were allelic.

The *NPR1* gene not only controls the onset of systemic resistance, but also was found to affect local acquired resistance ("LAR"), the ability of plants to restrict the spread of virulent pathogen infections. In *npr1* mutant plants, the virulent pathogen *P.s. maculicola* ES4326 grows to a greater extent and spreads further beyond the initial site of invasion than in the wild-type plants. The effects of the impaired SAR and LAR in *npr1* mutants is also evident when various strains of *Peronospora parasitica* were tested. Disease symptoms (i.e., downy mildew) were observed after infection by strains of *P. parasitica* to which the wild-type parental line of *Arabidopsis* is resistant, showing the break down of the "natural" resistance in the *npr1* mutants. The effects of the *npr1* mutations appeared to be specific to the defense response. No significant morphological phenotypes were observed in three allelic *npr1* mutants, *npr1-1*, *npr1-2*, *npr1-3*. However, when grown on medium containing a high concentration of SA (0.5 mM), the growth of all three *npr1* mutants was arrested at the cotyledon stage, and the seedlings were bleached. Wild-type plants were observed to grow normally in the presence of 0.5 mM SA.

The phenotypes of the *npr1* mutants clearly demonstrated the biological significance of the *NPR1* gene of *Arabidopsis thaliana* in controlling the defense response against a broad spectrum of pathogens.

The *NPR1* gene was cloned using a map-based positional cloning strategy. The location of *NPR1* on the *Arabidopsis* genome was first delimited to a 7.5-kilobase (kb) region contained on cosmid clones 21A4-4-3-1, 21A4-6-1-1, 21A4-P5-1, 21A4-P4-1, and 21A4-2-1 by its ability to complement the *npr1* mutant. An SA-inducible 2.0-kb RNA transcript encoded within this 7.5-kb region corresponding to *NPR1* was identified by RNA blot analysis. Isolation of this acquired resistance gene facilitates the cloning of AR genes from plants of agricultural or economic importance. For example, engineering ectopic expression of AR genes (for example, an *NPR* gene) in crop plants, which is useful for providing novel strategies for creating plants with enhanced resistance to pathogen infection.

There now follows a description of the cloning of an *Arabidopsis* AR gene, *NPR1*. A

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description is also provided of the cloning of the *NPR1* homolog from *Nicotiana glutinosa*. These examples are provided for the purpose of illustrating the invention, and should not be construed as limiting.

Genetic Analysis of SAR in *Arabidopsis* and the Isolation of *npr1* Mutants

5           Using *Arabidopsis thaliana*, components of the signalling pathway in SAR downstream of SA and INA induction have been identified. Specifically, we sought *Arabidopsis* mutants that did not express *PR* genes in the presence of added SA or INA. Because there is no visible phenotype known to be associated with such mutants, transgenic *Arabidopsis* plants were generated which expressed  $\beta$ -glucuronidase (*GUS*) under the control  
10 of the *Arabidopsis*  $\beta$ -1,3-glucanase (*BGL2*) promoter (Dong et al., *Plant Cell* 3:61-72, 1991). The *BGL2* gene is one of the *PR* genes regulated by SA (Uknes et al., *Plant Cell* 4:645-656, 1992). Briefly, seed from the transgenic line (*BGL2-GUS*) were mutagenized with ethyl methanesulfonate (EMS), and the resulting mutants were screened after SA or INA treatment for aberrant expression of *GUS*. The results of these screenings showed that high levels of  
15  $\beta$ -glucuronidase (*GUS*) activity could be assayed in a single well of a ninety-six well microtiter plate using a single leaf from a plant that had been grown for two weeks on plates containing SA or INA. Screens were performed for *Arabidopsis* mutants that either expressed the *BGL2-GUS* reporter constitutively in the absence of SA or INA treatment or that failed to express the reporter gene following treatment with SA or INA. These screens  
20 led to the identification of a series of mutants called *cpr* and *npr* (constitutive expresser of *PR* genes and for non-expresser of *PR* genes, respectively) which define genes that are involved both in the regulation of *BGL2* specifically and SAR in general (Bowling et al., *Plant Cell* 6:1845-1857, 1994; Cao et al., *Plant Cell* 6:1583-1592, 1994).

Construction of *BGL2-GUS* Transgenic *Arabidopsis*

25           An *XbaI-SphI* fragment (2025 base pairs (bp)) containing 1746-bp of noncoding sequence upstream of the start codon of the *Arabidopsis BGL2* gene was fused at the ATG site to the coding region of the *Escherichia coli uidA* gene (referred to as the *GUS* gene) and transferred into the vector pBI101, which was then used to transform *Arabidopsis* ecotype Columbia (Valvekens et al., *Proc. Natl. Acad. Sci. USA* 85:5536-5540, 1988). Plants

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homozygous for the *BGL2-GUS* construct were identified on the basis that progeny of these plants were resistant to kanamycin and the presence of the transgene that was detected using Southern hybridization.

Mutagenesis of the *BGL2-GUS* Transgenic Line

- 5 Mutagenesis was performed in the *BGL2-GUS/BGL2-GUS* transgenic line by exposing ~36,000 seeds to 0.3% ethyl methanesulfonate for eleven hours. Seeds were sown, and the plants were allowed to self-fertilize to produce  $M_2$  seeds, which were collected in twelve independent pools.

Identification of the *npr1-1* Mutant

- 10 The  $M_2$  seeds were germinated on MS medium with the addition of 0.8% agar, 0.5 mg/mL Mes (2-(*N*-morpholino)ethane-sulfonic acid), pH 5.7, 2% sucrose, 50  $\mu$ g/mL kanamycin, and 100  $\mu$ g/mL ampicillin. Either 0.5 mM salicylic acid (SA) or 0.1 mM INA was added to induce systemic acquired resistance (SAR). After incubation for fifteen days, each seedling to be assayed was numbered, and a single leaf was then removed from each
- 15 seedling and put into the corresponding sample well of a ninety-six-well microtiter plate that contained 100  $\mu$ L of  $\beta$ -glucuronidase (GUS) substrate solution (50 mM  $\text{Na}_2\text{HPO}_4$ , pH 7.0, 10 mM  $\text{Na}_2\text{EDTA}$ , 0.1% Triton X-100, 0.1% sarkosyl, 0.7  $\mu$ L/mL  $\beta$ mercaptoethanol, and 0.7 mg/mL 4-methylumbelliferyl  $\beta$ -D-glucuronide). After all the samples were collected, the microtiter plate was placed under vacuum for two minutes to infiltrate the samples and then
- 20 incubated at 37°C overnight. Samples were examined for the fluorescent product of GUS activity (4-methylumbellifone) using a long-wavelength UV light. Those seedlings which showed no GUS activity were identified on the MS plate and transplanted to soil for seed setting. This procedure was repeated in the progeny of these putative mutants to ensure that the mutant phenotype was heritable and to identify the homozygous mutants. Of 13,468  $M_2$
- 25 plants tested, 181 did not exhibit GUS activity in the presence of either SA or INA. In the  $M_3$  generation, 77 of 139 lines tested maintained a mutant phenotype for GUS activity, with 76 nonresponsive to both SA and INA and one line nonresponsive to SA but responsive to INA.

Three classes of mutations were predicted to be carried by the mutants that were nonresponsive to SA or INA treatment: (1) mutations in regulatory genes which not only

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affect expression of the transgene, but also the endogenous *PR* genes; (2) mutations in the promoter of the transgene which affect the responsiveness of *BGL2-GUS*, but not that of the endogenous *PR* genes to SA and INA; and (3) mutations in the coding region of the *GUS* gene which abolish the enzymatic activity of GUS, but not the transcription of *GUS* mRNA.

- 5 To distinguish between these classes, the expression of endogenous *PR* genes was analyzed in the  $M_3$  generation. Regulatory gene mutants should be readily distinguished in the  $M_3$  generation by an aberrant level of expression of other SAR-related *PR* genes.

RNA gel blot analysis was performed with these 77 mutant lines to identify those with modified expression of *PR* genes. The expression of the *Arabidopsis* mitochondrial  
10  $\beta$ -ATPase gene served as a control for sample loading. Among the 77 mutant lines, six were found to have reduced expression of the endogenous *PR* genes to some degree (class 1); three showed aberrant expression only in *BGL2-GUS* (class 2); and fourteen were found to have reduced GUS activity but normal transcription of *BGL2-GUS* (class 3). One class 1 mutant  
15 (*npr1-1*) exhibited a dramatic reduction in expression of the *GUS*, *BGL2*, and *PR-1* genes compared to the wild-type in the presence of SA or INA. Therefore, *npr1-1* was selected for further study.

The *npr1-1* mutant was tested for the induction of *PR-5*, another *PR* gene that has been cloned in *Arabidopsis* (Uknes et al., *Plant Cell* 4:645-656, 1992), and a similar reduction in expression was observed. The reduction in *PR* gene expression after SA or INA  
20 treatment was quantified for *npr1-1* relative to the parent *BGL2-GUS* line (representing the wild-type). In *npr1-1*, the expression of both *GUS* and *BGL2* was ten-fold lower than that of the wild-type and that of *PR-5* was five-fold lower. The most dramatic reduction was observed for *PR-1* which was twenty-fold lower than the wild-type.

#### Quantitative GUS Assays Using *npr1-1*

- 25 To measure accurately the level of GUS activity, a quantitative GUS assay was performed on *npr1-1* plants and the wild-type *BGL2-GUS* plants grown in the presence of either SA or INA, or in the absence of both. In the absence of an inducer, the background level of GUS activity was five-fold lower in the *npr1-1* mutant than in the wild-type. Wild-type plants grown in the presence of 0.5 mM SA showed a fifty-two-fold increase in



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GUS activity compared to the uninduced plants, whereas in the SA-induced *npr1-1* plants, the increase in GUS activity was only seven-fold. Moreover, the induction by 0.1 mM INA was forty-eight-fold for the wild-type versus five-fold for *npr1-1*. Thus, while GUS activity in the SA- or INA-treated *npr1-1* plants was somewhat induced, the activity was at most only slightly higher than the background level of the untreated wild-type.

#### Genetic Analysis of the *npr1-1* Locus

A backcross of *npr1-1/npr1-1* with its wild-type parent (*NPR1/NPR1* in the *BGL2-GUS* background) resulted in  $F_1$  progeny (*NPR1/npr1-1*, sixteen plants were tested) with the same pattern of GUS staining (using 5-bromo-4-chloro-3-indolyl glucuronide [XGluc] as the substrate) observed in the wild-type after SA or INA treatment. GUS staining was not detected in the SA- or INA-treated *npr1-1/npr1-1* homozygous plants even after two days of incubation at 28°C. Self-fertilization of the  $F_1$  plants produced  $F_2$  progeny that segregated for GUS activity, intense staining or complete absence of staining, which were present with a ratio of 219:64 among the 283  $F_2$  plants examined, demonstrating that the mutant phenotype is recessive and due to a single nuclear mutation ( $\chi^2=0.86$ ;  $P>0.1$ ).

#### SA-, INA-, and Avirulent Pathogen-Induced Protection Against *Pseudomonas syringae* pv *maculicola* ES4326 Infection in Wild-Type and *npr1-1*

To examine whether the lack of SA- or INA-induced *PR* gene expression would affect SAR protection against a virulent pathogen infection, fifteen-day-old wild-type and *npr1-1* plants were treated with either 1 mM SA or 0.65 mM INA, and two days later were exposed to a *P.s. maculicola* ES4326 bacterial suspension. Significant protection was observed in the SA- or INA-treated wild-type plants with less than ten percent of plants showing slight yellowing. Chlorotic lesions developed in about ninety percent of the untreated wild-type control plants not pretreated with SA or INA. However, such SA- or INA-induced protection was not observed in *npr1-1* mutant plants. Chlorotic lesions were clearly seen in over ninety-percent of untreated and at least eighty-percent of SA- or INA-treated plants. The symptoms on *npr1-1* were also more severe than on the wild-type plants. Treatment with only 1 mM SA, 0.65 mM INA, or surfactant (0.01% Silwet-77, used for the bacterial infection) had a

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minimal effect on both the wild-type and the *npr1-1* plants.

The growth of *P.s. maculicola* ES4326 was measured in both wild-type and *npr1-1* plants that had been treated with water, SA, or INA two days before *P. s. maculicola* ES4326 infection. Leaves were collected 0, 0.5, 1.0, 2.0, and 3.0 days after bacterial infiltration. For the untreated wildtype plants, *P.s. maculicola* ES4326 proliferated 10,000-fold during this time period. However, for SA- or INA-treated wild-type plants, the growth of *P.s. maculicola* ES4326 was only about ten-fold, 1000 times lower than the untreated control. A Student's *t* test of the difference between the means at the three-day time point clearly showed that growth of the pathogen is inhibited in the wild-type plants treated with SA or INA compared to those sprayed with water ( $P < 0.001$ ). Such a dramatic difference in *P.s. maculicola* ES4326 growth, which resulted from SAR protection, was not observed in the *npr1-1* plants, where a Student's *t* test showed no statistically difference in growth after three days for all conditions ( $P > 0.05$ ); the growth of *P.s. maculicola* ES4326 in *npr1-1* plants was similar for mock-treated and either SA- or INA-treated plants. Comparing the untreated *npr1-1* plants with the untreated wild-type, the level of *P.s. maculicola* ES4326 appeared to have reached saturation one day earlier in the mutant than in the wild-type. Moreover, the difference in *P.s. maculicola* ES4326 growth between the SA- or INA-treated wild-type and *npr1-1* was 500- to 1000-fold.

To test the response to an avirulent pathogen, the *npr1-1* plants were infiltrated with *P.s. maculicola* ES4326 carrying an avirulence gene *avrRpt2* as described by Dong et al. (*Plant Cell* 3:61-72, 1991) and Whalen et al. (*Plant Cell* 3:49-59, 1991). A typical HR was observed in these *npr1-1* plants as characterized by the rapid appearance of necrotic lesions, detection of autofluorescence in the cell wall regions of the infected cells, and inhibited growth of *P.s. maculicola* ES4326/*avrRpt2*. The ability of this avirulence gene to induce SAR in *npr1-1* plants was then tested. To distinguish the inducing bacterial strain from the challenging strain, the bean pathogen *Pseudomonas syringae* pv *phaseolicola* strain NPS3121 (*P.s. phaseolicola* NPS3121; (Lindgren et al., *J. Bacteriol.* 168:512-522, 1986)) containing the *avrRpt2* gene was used to induce SAR in both the *npr1-1* and wild-type plants. *P.s. phaseolicola* NPS3121 by itself caused no disease symptoms or visible HR on *Arabidopsis*

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ecotype Columbia, while *P.s. phaseolicola* NPS3121/*avrRpt2* elicited a strong HR (Yu et al., *Mol. Plant-Microbe Interact.* 6:434-443, 1993). Three days after the inoculation, uninfected leaves on the same plants were challenged with the virulent pathogen *P.s. maculicola* ES4326, and the growth of *P.s. maculicola* ES4326 in the plants was measured. A significant reduction in bacterial growth was observed in the wild-type plants pre-inoculated with *P.s. phaseolicola* NPS3121/*avrRpt2* compared to the mock treated samples (300-fold); however, no difference in *P.s. maculicola* ES4326 growth was detected in *npr1-1* plants.

Disease Symptoms and BGL2-GUS Expression Induced by *P.s. maculicola* ES4326 Infection in Wild-Type and *npr1-1*

*P.s. maculicola* ES4326 was able to establish infection in SA-, INA-, and avirulent pathogen-treated *npr1-1* plants as well as in the untreated plants. The lesions formed on the untreated mutant plants and the untreated wild-type were further compared. For this purpose, the *P.s. maculicola* ES4326 suspension was infiltrated into four-week-old wild-type and *npr1-1* leaves. The injection was controlled so that only half of the leaf was infiltrated with the bacteria. This could be monitored by the soaking appearance of the half-leaf. Forty-eight hours following infiltration, chlorotic lesions were visible on the wild-type leaves. These lesions were normally confined to the infiltrated halves of the leaves as defined by the midrib vein. Different lesions were observed on the *npr1-1* leaves, where the lesions were more diffuse and often spread into the uninfected halves of the leaves. Sampling of twelve leaves from both wild-type and *npr1-1* plants revealed significant growth of the bacteria in the uninoculated half of eleven *npr1-1* leaves compared to none of the wild-type leaves.

For the leaves infected with *P.s. maculicola* ES4326, the pattern of *BGL2-GUS* expression was examined by X-Gluc staining. In a wild-type leaf, a high level of GUS staining was detected in the peripheral region of the lesion. In contrast, no significant GUS activity was detected on the *npr1-1* leaf, where the lesion was more extensive than on the wild-type.

Conclusions About *npr1-1*

The data described above indicates that *npr1-1* harbors a *trans*-acting mutation(s)

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affecting the response to SA and INA. The possibility of *npr1-1* being a mutant affecting the uptake of exogenously applied SA or INA is ruled out by the observation that the expression of *PR1* induced by *P.s. maculicola* ES4326, instead of by exogenously applied SA or INA, is also reduced in the *npr1-1* mutant. The failure of SA or INA to protect the *npr1-1* mutant from infection by *P.s. maculicola* strain ES4326 (in contrast to the protection observed in wild-type plants) indicated that the *npr1-1* mutation blocks SA or INA induction of resistance. Even though the HR elicited in the *npr1-1* mutant by bacteria carrying the avirulence gene *avrRpt2* was similar to that described previously in wild-type plants (Dong et al., *Plant Cell* 3:61-72, 1991; Whalen et al., *Plant Cell* 3:49-59, 1991), the HR-induced SAR protection against infection by the virulent pathogen *P.s. maculicola* ES4326 was absent in the *npr1-1* plants. This indicated that *npr1-1* is a mutation that prevents the onset of SAR. These phenotypes of the *npr1-1* mutation indicated that the function of the wild-type *NPR1* gene is to qualitatively and quantitatively regulate the expression of SA- and INA-responsive *PR* genes.

Genetic analysis of the progeny of an *npr1-1/npr1-1* X *NPR1/NPR1* backcross indicated that a single recessive nuclear mutation determines the "nonexpresser of *PR* genes" phenotype of the *npr1-1* mutant. This also indicated that the *NPR1* gene acts as a positive regulator of SAR responsive gene induction. While the gene could be a negative regulator which is inactivated by SAR induction, a mutation abolishing such regulation would likely be dominant. Furthermore, the fact that a single mutation (that is, *npr1-1*) affects the responsiveness of this mutant to SA-, INA-, and pathogen induction indicated that SA, INA, and pathogens activate a common pathway that leads to the expression of *PR* genes.

#### Identification of the *Arabidopsis npr1-2* and *npr1-3* Mutants

To identify novel *Arabidopsis* mutants that negatively affect the induction of SAR, an alternative mutant screening strategy was employed.

We have observed that the final density to which the virulent pathogen *P.s. maculicola* ES4326 will grow in an *Arabidopsis* leaf is directly related to the dose at which *P.s. maculicola* ES4326 was infiltrated. The observed phenotypes of two additional types of *Arabidopsis* mutants also supported this conclusion. Specifically, a series of *Arabidopsis*

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mutants were identified that accumulated reduced levels of the phytoalexin called camalexin, a phytoalexin that has been found in significant quantities in *Arabidopsis* (Glazebrook and Ausubel, *Proc. Natl. Acad. Sci. USA* 91:8955-8959, 1994; Tsuji et al., *Plant Physiol.* 98:1304-1309, 1992). Importantly, *P.s. maculicola* ES4326 formed disease lesions and grew to higher titers on some of these *pad* (phytoalexin deficient) mutants when inoculated at doses below the threshold dose required to give disease symptoms in wild-type plants. Similarly, *npr1-1* mutants exhibited a similar enhanced susceptibility phenotype as *pad* mutants (Cao et al., *Plant Cell* 6:1583-1592, 1994).

Based on these findings that *pad* and *npr* mutants were more susceptible to low dose *P.s. maculicola* ES4326 infection than wild-type plants, a screen was performed to isolate additional *eds* (enhanced disease susceptibility) mutants (Glazebrook et al., *Genetics* 143:973-982, 1996). Two leaves of M2 generation mutagenized *Arabidopsis* plants were infected at a dose of strain *P.s. maculicola* ES4326 at which wild-type plants showed very weak symptoms manifested as small chlorotic spots three days after infection, whereas *pad* and *npr1* mutants showed large areas of chlorosis. A total of fifteen *eds* mutants that reproducibly allowed at least one half log more growth of *P.s. maculicola* ES4326 as compared to wild-type were identified among 12,500 plants screened. Because some *pad* mutants as well as *npr1-1* mutants have the same enhanced susceptibility phenotype with respect to *P.s. maculicola* ES4326 as the *eds* mutants (Glazebrook et al., *Genetics* 143:973-982, 1996), the fifteen *eds* mutants were tested to determine whether they synthesized wild-type levels of camalexin in response to infection by *P.s. maculicola* ES4326 (*pad* phenotype) and whether *PR1* gene expression can be induced by salicylic acid (*npr1-1* phenotype). The results of these analyses showed that two of the *eds* mutants exhibited an *npr1*-like phenotype. Genetic complementation analysis showed that these two mutations are allelic to *npr1-1*. These two mutants were re-named *npr1-2* and *npr1-3*.

#### Map-Based Positional Cloning of the *Arabidopsis* *NPR1* Gene

To map the *NPR1* gene, a genetic cross was made between the *npr1-1* mutant (present in the Columbia ecotype (Col-O) which carried the *BGL2-GUS* reporter gene) and the wild-

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type (present in Landsberg *erecta* ecotype (La-*er*) which carried the *BGL2-GUS* reporter gene). F3 families from this cross that are homozygous for this mutation at the *NPR1* locus were identified by their lack of expression of *BGL2-GUS* when grown on plates containing 0.1 mM INA. Expression of the GUS reporter gene was detected by a chromatographic assay of GUS activity using the substrate 5-bromo-4-chloro-3-indolyl glucuronide according to standard techniques (Cao et al., *Plant Cell* 6:1583-1592, 1994 and Jefferson *Plant Mol. Biol. Reporter* 5:387-405, 1987). The leaf tissues of these F3 *npr1-1* progeny pools (from thirty to forty two-week-old seedlings) were collected and frozen in liquid nitrogen. From the frozen tissues, genomic DNA preparations were made as described by Dellaporta et al. (*Plant Mol. Biol. Reporter* 1:19-21, 1983) and used to determine the genotypes of various restriction fragment length polymorphism (RFLP) and codominant amplified polymorphic sequence (CAPS) (Konieczny and Ausubel, *Plant J.* 4:403-410, 1993) markers. The frequencies of recombination between the *NPR1* locus and the RFLP and CAPS markers were used to determine the position of the *NPR1* gene according to conventional methods.

As shown in Fig. 1, the *NPR1* gene was mapped to *Arabidopsis* chromosome I, and found to reside between the CAPS marker GAP-B (~22.70 cM on the centromeric side of the *NPR1* gene) and the RFLP marker m315 (~7.58 cM on the telomeric side of the *NPR1* gene).

To carry out fine mapping of the *NPR1* gene, new CAPS and RFLP markers were generated from clones that the genetic maps in the AtDB database (<http://genome-www.stanford.edu/Arabidopsis/>) showed were located between *GAP-B* and *m315*. Cosmid *g4026* (CD2-28, *Arabidopsis* Biological Resource Center, The Ohio State University, Columbus, OH) was cut with the restriction enzyme *EcoRI* and a 4-kb fragment was used to identify a polymorphism between Col-0 and La-*er* after the genomic DNA was digested with *HindIII*. Using this RFLP marker, six heterozygotes were detected among the twenty-three F3 families that were heterozygous at *GAP-B*. None were found among the seven F3 families that were heterozygous at *m315*. Therefore, *g4026* is ~5.92 cM on the centromeric side of the *NPR1* gene. Cosmid *g11447* (obtained from the collection of Dr. Howard Goodman at the Massachusetts General Hospital (Nam et al., *Plant Cell* 1:699-705, 1989)) was used to generate a CAPS marker. End-sequences of an 0.8-kb *EcoRI* fragment were used to design

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PCR primers (primer 1: 5' GTGACAGACTTGCTCCTACTG 3' (SEQ ID NO:15); primer 2: 5' CAGTGTGTATCAAAGCACCA 3' (SEQ ID NO:16) which amplified a fragment displaying a polymorphism when digested with the *EcoRV* restriction enzyme. Among the 436 *npr1-1* F3 progeny tested using this newly generated CAPS marker, seventeen heterozygotes were discovered. Since these heterozygotes were all homozygous Col-0 for the *GAP-B* locus, the *gll447* marker was placed ~1.95 cM on the telomeric side of the *NPR1* gene.

There are a number of RFLP markers mapped between *gll447* and *g4026*. The first marker tested was *m305* (designated CD1-11, *Arabidopsis* Biological Resource Center, the Ohio State University, Columbus, OH (Chang et al., *Proc. Natl. Acad. Sci., USA* 85:6856-6860, 1988)). A 5-kb *EcoRI* fragment isolated from the *m305* lambda clone was further subcloned using *SalI/XbaI* and the end-sequences of a 1.6-kb fragment were used to design PCR primers (primer 1: 5' TTCTCCAGACCACATGATTAT 3' (SEQ ID NO:17); primer 2: 5' TGAAGCTAATATGCACAGGAG 3' (SEQ ID NO:18)). The resulting PCR fragment amplified using these primers was digested with *HaeIII* to detect a polymorphism. Among the 305 *npr1-1* progeny examined using this *m305* CAPS marker, no heterozygotes were found, indicating that the *m305* marker lies extremely close to *NPR1*.

A partial physical map of chromosome I (<http://cbil.humgen.upenn.edu/~atgc/ATGCUP.html>) showed a YAC contig that includes *m305*. The YACs in this contig, as well as left-end-fragments of YAC clones yUP19H6, yUP21A4, and yUP11H9 were obtained from Dr. Joseph Ecker at the University of Pennsylvania. The yUP19H6L end-probe was found to detect an *RsaI* polymorphism, and five recombinants were identified among the *GAP-B* recombinants on the centromeric side of the *NPR1* gene (as shown by the vertical arrows in Fig. 1). The yUP11H9L end-probe was found to detect a *HindIII* polymorphism, and one heterozygote was found among the seventeen recombinants for *gll447* on the telomeric side of the *NPR1* gene (as shown by a vertical arrow in Fig. 1). Since yUP11H9L hybridized with the yUP19H6 YAC clone, these results showed that the *NPR1* gene is located on yUP19H6. In addition to *m305*, yUP21A4L

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(detects an *EcoRI* polymorphism) and *g8020* (a 1.3-kb *EcoRI* fragment that detects a *HindIII* polymorphism) were found to be very closely linked to the *NPR1* gene with no recombinants identified. *m305*, yUP21A4L, and *g8020* all hybridized to the yUP19H6 YAC clone, further supporting the conclusion that yUP19H6 contains the *NPR1* gene.

5    Construction of a Cosmid Library from the YAC Clone yUP19H6

A genomic DNA preparation was made from the yeast strain containing the YAC clone yUP19H6. This DNA was partially digested with the restriction enzyme *TaqI*, size selected on a 10-40% sucrose gradient, and cloned into the *ClaI* site of the binary vector, pCLD04541 (obtained from Dr. Jonathan Jones (Bent et al., *Science* 265:1856-1860, 1994)).

10   The pCLD04541 vector is a standard transformation vector used for preparing cosmid libraries. This plasmid carries a T-DNA polylinker region, and tetracycline and kanamycin resistance markers.

The cosmid clones were packaged into bacteriophage lambda particles using a commercial packaging extract (Gigapack XL, Stratagene, LaJolla, CA) and introduced into *E.*  
15   *coli* strain DH5 $\alpha$  according to the instructions of the supplier. The resulting library was found to contain approximately 40,000 independent clones.

Generation of a Cosmid Contig Containing the *NPR1* Gene

The cosmid library generated from the yeast strain containing yUP19H6 was plated (1,500 cfu/plate) on LB medium agar (containing 5  $\mu$ g/mL of tetracycline to select for the  
20   presence of pCLD04541) and incubated at 37°C overnight. Colonies were lifted onto membranes (GeneScreen, Du Pont, New England Nuclear) and hybridization was carried out according to the protocol described by the manufacturer. The library was probed with 5-kb *EcoRI*, 6.5-kb *EcoRI/XhoI*, and a 1.3-kb *EcoRI* fragments prepared from *m305*, yUP21A4L, and *g8020*, respectively. The colonies that hybridized with these probes were identified and  
25   purified according to conventional methods. Cosmid DNA preparations were made from these positive clones using the alkaline lysis method described by Sambrook et al. (*Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, New York, 1989), and the inserts were analyzed by *HindIII* restriction digestion and Southern hybridization using the probes stated above. The cosmids were found to form a single cosmid contig spanning



approximately 80-kb of *Arabidopsis* DNA. Three of the five recombinants for yUP19HL were shown to be heterozygous at an RFLP marker detected by cosmid clone *m305-3-1* (a 5-kb *HindIII* fragment) at the centromeric side of the contig, while the single heterozygote detected by *g8020* marker was also detected by the cosmid clone *g8020-6-3* (a 1.25-kb *HindIII* fragment) at the telomeric side of the contig. This showed that the cosmid contig contained the *NPR1* gene (Fig. 1). From this contig, fourteen cosmids which each have a minimum of 10-kb overlap with the neighboring clones (Fig. 1) were chosen to transform *npr1* mutant plants in complementation experiments.

#### Complementation of the *npr1* Mutations

The cosmid clones contained in the *E. coli* strain DH5 $\alpha$  were transferred into the *Agrobacterium tumefaciens* strain GV3101 (pMP90) (Koncz and Schell, *Mol. Gen. Genet.* 204:383-396, 1986) by conjugation using the helper strain MM294A (pRK2013) (Finan et al., *J. Bacteriol.* 167:66-72, 1986). The resulting *A. tumefaciens* conjugants were selected using 50  $\mu$ g/mL kanamycin and 50  $\mu$ g/mL gentamycin. The *A. tumefaciens* strains carrying those fourteen cosmid clones were transformed into *npr1-1* (Cao et al., *Plant Cell* 6:1583-1592, 1994) and *npr1-2* (Glazebrook et al., *Genetics* 143:973-982, 1996) using a vacuum infiltration method described by Bechtold et al. (*C.R. Acad. Sci. Paris, Life Sciences* 316:1194-1199, 1993). The integrity of the cosmid clones in the *A. tumefaciens* cultures used for transformation were examined by Southern analysis.

Transformants of *npr1-2* were grown (22°C in fourteen hours of light) and selected on MS medium agar (Murashige and Skoog, *Physiol Plant.* 15:473-497, 1962) containing 2% sucrose, 50  $\mu$ g/mL kanamycin, and 100  $\mu$ g/mL ampicillin. Kanamycin-resistant transformants which developed true leaves and healthy roots were transplanted to soil. After two weeks of growth in soil at 22°C in fourteen hours of light per day, leaves were collected from three transformants of each cosmid clone and soaked in 0.5 mM INA solution for twenty-four hours at 22°C in fourteen hours of light per day. Leaf tissues were then collected and frozen in liquid nitrogen. Total RNA was extracted from these leaf tissues, and an RNA blot was prepared as described by Cao et al. (*Plant Cell* 6:1583-1592, 1994). The blot was probed with a *PR1*-specific probe (a PCR product obtained by amplifying genomic

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*Arabidopsis* DNA with *PR1*-specific primers (sense primer 5' GTAGGTGCTCTTGTCTTCCCC3' (SEQ ID NO:19); anti-sense primer 5'CACATAATTCCCACGAGGATC3' (SEQ ID NO:20)).

In control experiments, the wild-type parental line showed the induction of the *PR1* gene by INA, while the *npr1-2* mutant exhibited no induction of *PR-1* gene expression. *Npr1-2* transformants containing cosmids (three for each cosmid) 21A4-6-1-1, 21A4-P5-1, 21A4-4-3-1, and 21A4-2-1 showed strong induction of *PR1* by INA, while *npr1-2* transformants containing other clones (for example, M305-2-3, M305-3-9, and 21A4-3-1) displayed no induction. Variations were observed in the intensity of RNA bands among three individual transformants sampled for each cosmid clone. These variations were likely to be the result of "position-effects," the effect of the insertion site in the chromosome on the expression of the transgene. Cosmid clones 21A4-4-3-1, 21A4-6-1-1, 21A4-P5-1, and 21A4-2-1 restored the ability of the *npr1-2* mutant to respond to INA induction and, therefore, complemented the *npr1-2* mutation. Examples of INA induced *PR1* are shown in Fig. 2A.

Transformants carrying each cosmid were also tested for SA induction of *PR1* expression by RNA blot analysis. Examples of SA induction are shown in Figure 2A. The wild-type parental line exhibited a high level of *PR1* gene induction by SA, whereas the *npr1-2* mutant exhibited only a minor induction (Fig. 2A). Transformants of the *npr1-2* mutant containing cosmids 21A4-6-1-1, 21A4-P5-1, 21A4-4-3-1, and 21A4-2-1 showed induction of *PR1* by SA, while those containing the other clones displayed little induction.

As shown in Fig. 1, these four clones share a common region of 7.5-kb. Transformants of cosmid 21A4-P4-1 were not available when the experiment described above was conducted. However, according to its relative position, it is expected that this clone can also complement the *npr1-2* mutation.

The same fourteen cosmid clones were also transformed into the *npr1-1* mutant. Since the *npr1-1* mutant carries the *BGL2-GUS* reporter and the kanamycin resistance gene (NPTII), transformants of the cosmid clones could not be selected using kanamycin. Instead, transformants that complemented the *npr1-1* mutation were selected directly by growing the

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seeds collected from the *npr1-1* plants infiltrated with *A. tumefaciens* on a high concentration of SA (0.5 mM). Those plants that developed green leaves were transplanted to another plate containing 0.1 mM INA, and GUS activity was measured one week after transplanting.

To measure GUS activity, seedlings were numbered, and a single leaf was removed  
5 from each plant and placed in a microtiter well containing 100  $\mu$ L of GUS substrate (4-methylumbelliferyl  $\beta$ -glucuronide) in a solution as described previously (Cao et al., *Plant Cell* 6:1583-1592, 1994; Jefferson, *Plant Mol. Biol. Reporter* 5:387-405, 1987). After an overnight incubation at 37°C, the fluorescent product of GUS activity was examined under a long wavelength UV light. As controls, twelve seedlings of the wild-type parental line  
10 (*BGL2-GUS*) were tested, and all showed intense fluorescence after growth on SA and INA. Twelve seedlings of the *npr1-1* mutant (*BGL2-GUS*) were also included in the experiment, and none displayed any increase in fluorescence. From this experiment, nine seedlings carrying cosmid 21A4-P4-1, five carrying 21A4-P5-1, and six carrying 21A4-2-1 were found to have high levels of fluorescence, i.e., GUS activity, and none of the seedlings from other  
15 cosmid clones were identified through this selection. Direct identification of putative complementing transformants in the *npr1-1* mutant plants by the cosmid clones 21A4-P4-1, 21A4-P5-1, and 21A4-2-1 as in the transformation experiment using the allelic *npr1-2* mutant (where all transformants were first selected by kanamycin resistance before identification of the transformants that could complement the *npr1-2* mutation using RNA blot analysis)  
20 further supported the conclusion from complementation experiments with *npr1-2* that the 7.5 kb region shared by cosmids 21A4-4-3-1, 21A4-6-1-1, 21A4-P5-1, 21A4-P4-1, and 21A4-2-1 complemented *npr1* mutations, and that this 7.5-kb region contained the *NPR1* gene.

In addition to reduced *PR* gene expression, plants with *npr1* mutations display susceptibility to virulent pathogens even after SAR induction. These mutant phenotypes  
25 were also complemented by the cosmids described above. For example, as shown in Figure 2B, infection by the bacterial pathogen Psm ES4326 caused visible disease symptoms three days after infection. While the disease symptoms in the wild-type plants and the complemented *npr1-1* transformants were well-confined to the site of pathogen infiltration (the left side of the leaf), the lesions in the *npr1-1* plants were found to spread beyond the site  
30 of infiltration. In addition, when the dosage of infecting bacteria was reduced 10-fold, severe

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disease symptoms were only observed in the *npr1-1* mutant (leaves on the right). This experiment showed that 21A4-4-3-1 complemented the enhanced susceptibility to Psm ES4326 displayed by *npr1-1*.

5 The expression of the *BGL2-GUS* gene was also analyzed in the same leaves after examination of the disease symptoms (Fig. 2B). Strong GUS expression (blue staining) was detected in the marginal regions of the well-confined lesions in the wild-type plants, but was absent from the diffuse lesions in the *npr1-1* plants. Reporter gene expression was restored in complemented transformants.

10 In addition to these visual observations, as shown in Fig. 2C, bacterial growth of Psm ES4326 was measured quantitatively in wild-type, *npr1-2*, and an *npr1-2* transformant with a complementing cosmid (21A4-P5-1). Plants were treated with 0.65 mM INA seventy-two hours prior to Psm ES4326 infection ( $OD_{600} = 0.001$ ). Infection of *Arabidopsis* with Psm ES4326 was performed according to standard methods (Bowling et al., 1994; *supra*, Cao et al., *supra*, 1994; Glazebrook et al., *supra*, 1996). Samples were taken before infection and  
15 one, two, and three days after infection. Six to eight samples were taken for each time point analyzed and colony-forming units of Psm ES4326 were determined per leaf disc. Complete inhibition of Psm ES4326 growth was observed in the wild-type plants following INA treatment three days prior to infection, whereas an approximate 10-fold decrease in Psm ES4326 growth was observed in the *npr1-2* mutant subjected to the same treatment. The  
20 growth of Psm ES4326 was also halted in the complemented transformants after INA treatment. Lower bacterial growth (as great as  $10^3$ -fold) was observed even in the water-treated transformants compared to the water-treated wild-type (Fig. 2C) and the water-treated transformants carrying noncomplementing cosmids. This enhanced resistance may result from the increased *NPR1* mRNA levels in these complemented transformants.

25 A test of resistance to a fungal pathogen, *P. parasitica* NOCO, was also performed to verify complementation of the *npr1-1* mutation. Infection of *Arabidopsis* with *P. parasitica* NOCO was performed according to standard methods (Bowling et al., *supra*, 1994; Cao et al., *supra*, 1994; Glazebrook et al., *supra*, 1996). INA treatment (0.65 mM) was carried out seventy-two hours prior to infection with a spore suspension ( $3 \times 10^4$  spores/1 mL). Seven  
30 days post-infection, the disease symptoms were scored with respect to the number of

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conidiophores observed on each plant. A total of twenty to twenty-five plants were examined for each genotype with each treatment. Data were analyzed using the Mann-Whitney U-Tests (Sokal and Rohlf, *supra*). As shown in Fig. 2D, the results of these experiments indicated that INA-induced resistance to *P. parasitica* NOCO was restored in the transformants with the complementing cosmids.

#### Analyses of the 7.5-kb Region Containing the *NPR1* Gene

The 7.5-kb region identified by the cosmid complementation experiment was further analyzed using restriction enzymes. The resulting restriction map from this analysis is shown in Fig. 3. Three sets of subclones were made using *Hind*III, *Xba*I, and *Cla*I/*Xho*I digestions of the cosmid 21A4-P5-1, which has the 7.5-kb region located in the center of the insert, and ligated into the vector pBluescript II SK<sup>+</sup> (Stratagene, La Jolla, CA). The 7.5-kb region of interest was represented by five *Hind*III subclones with the approximate insert sizes 1.96-kb, 1.91-kb, 1.74-kb, 1.25-kb, and 0.50-kb. Subclones with larger inserts (*Xba*I: ~8.5-kb, ~8.5-kb, ~1.45-kb; *Cla*I/*Xho*I: ~10.0-kb, and ~5.1-kb) were also made to orient and connect these *Hind*III fragments.

A Southern blot containing the *Hind*III-digested genomic DNA samples from the wild-type parental line (*BGL2-GUS*) and the three *npr1* mutants was examined with probes generated from *Hind*III fragments made from the cosmid clone 21A4-P5-1. No significant difference in the restriction patterns was observed between the wild-type and all three *npr1* allelic mutants. Therefore, it is unlikely that these mutants carried a substantial deletion in the *NPR1* gene.

DNA fragments covering the 7.5-kb region were used to detect transcripts on a blot containing the polyA mRNAs made from four-week-old plants of the wild-type parental line and of the three *npr1* allelic mutants seventy-two hours after treatment of the plants with H<sub>2</sub>O or 0.65 mM INA and 2 mM SA. The polyA mRNA samples were prepared using Dynabeads (Dynal, Inc., Lake Success, NY) from seventy-five micrograms of total RNA according to the protocol provided by Dynal. From this analysis, only one ~2.0-kb mRNA was detected in the 7.5-kb region using probes made from the 0.5-kb and the adjacent 1.96-kb *Hind*III fragments. This mRNA represented a putative transcript of the *NPR1* gene. In addition, the intensity of this transcript was about two-fold higher in the INA/SA-induced samples compared to the

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H<sub>2</sub>O-treated controls as measured by a PhosphorImager and ImageQuant (Molecular Dynamics, Sunnyvale, CA). Thus, the expression of this transcript believed to represent mRNA of the *NPR1* gene was induced by INA/SA treatment. No significant difference in the pattern of expression was discovered between the wild-type and three *npr1* mutant alleles on this polyA RNA blot.

#### Sequence Analysis of the *NPR1* Gene

The initial sequencing analysis was carried out using pBluescript SK<sup>+</sup> clones of the five *Hind*III fragments as templates. The template DNA samples were prepared using Qiagen Plasmid Mini Kits (Qiagen Inc., Chatsworth, CA), and 0.6 µg of the template was used for each sequencing reaction and analyzed by an ABI automated sequencer.

M13-20 and M13 reverse primers were used to initiate the sequencing reactions of the *Hind*III fragments. Various restriction enzymes were then used to generate deletions in these *Hind*III subclones to analyze sequences more distal to the ends of the fragments. In addition, primers were designed to perform primer walking. The relative positions of these *Hind*III fragments were determined and gaps between these fragments were filled by sequencing analyses using *Xba*I-subclones of cosmid 21A4-P5-1 as templates. The sequence data were analyzed to identify restriction enzyme sites, to perform sequence alignment and to search for open reading frames using standard DNA analysis software (DNA Strider 1.1, MacVector 4.0.1, and GeneFinder). Using this software only one putative gene was found. Sequence data were also compared to the TIGR *Arabidopsis thaliana* DataBase (<http://www.tigr.org/tdb/at/at.html>). The results of this study identified an expression sequence tagged (EST) clone that showed homology with a portion of the 1.96-kb fragment. This portion of the 1.96-kb fragment was also identified as part of the gene recognized using GeneFinder software. The nucleotide sequence of the 7.5-kb genomic region encoding the *NPR1* gene product is shown in Fig. 4.

#### Isolation of *NPR1* cDNA Clones

A cDNA library that was constructed by Dr. Katagiri (and described in detail in Mindrinos et al., *Cell* 78:1089-1099, 1994) was screened using the 1.96-kb *Hind*III fragment as a probe. Bacterial cells (*E. coli* DH10B; GIBCO BRL, Gaithersburg, MD) containing

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cDNAs made from the aerial parts of one-month old wild-type *Arabidopsis* plants in vector pKEx4tr were plated (60,000 cfu/plate) on LB medium containing 100 µg/mL ampicillin, and the plates were incubated at 37°C for four and one-half hours. Colonies were lifted onto Colony/Plaque Screen membranes (NEN Research Product; Boston, MA), and then the  
5 membranes were placed onto an LB plate, with the colony side up. Both plates were incubated at 30°C for twelve hours. The membranes were autoclaved for one minute to lyse the cells and fix the DNA to the membrane. Hybridization was performed at 42°C in a solution containing 10% dextran sulfate, 50% formamide, 6X SSC, 5X Denhardt's, and 1% SDS; and the membranes were washed twice at 65°C in 2X SSC and 1% SDS. The positive  
10 colonies were purified through secondary and tertiary screens using identical conditions. One positive cloned was subsequently identified and designated pKExNPR1.

The cDNA inserts were excised from the vector using restriction enzymes *EcoRI* and *SacI*. Southern analysis was performed using probes made from the 1.96-kb (the 3'-end of the open reading frame) and the 0.5-kb (the 5'-end of the open reading frame) *HindIII*  
15 fragments to confirm homology of the cDNA clones. The nucleic acid sequence (SEQ ID NO:2) and deduced amino acid sequence (SEQ ID NO:3) of the acquired resistance protein termed NPR1 from *Arabidopsis thaliana* encoded by the 2.1-kb cDNA is shown in Fig. 5. Sequence analysis revealed that this cDNA contained sequences corresponding to those identified in the EST clone and deduced using the Gene Finder software.

20 The cDNA sequence was analyzed using the BLAST sequence analysis program. This analysis revealed that the NPR1 protein shared significant homology with ankyrin, including the region identified as the ankyrin-repeat consensus. In particular, as shown in Fig. 6A, the *NPR1* sequence contains two regions with significant homology to the mammalian ankyrin 3 gene. The sequence identities between *NPR1* (amino acids 323-371  
25 and 262-289) and ANK3 (amino acids 740-788 and 313-340) are 42% and 35%, respectively, and the sequence similarities are 59% and 57%, respectively. This ankyrin-repeat consensus has been identified in a diverse array of proteins including transcription factors, cell differentiation molecules, structural proteins, and proteins with enzymatic and toxic activities. This motif has been shown to function by mediating protein interactions.

30 Using the consensus sequence defined by Michaely and Bennett (*Trends in Cell*

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*Biology* 2:127-129, 1992) and Bork (Proteins: Structure, Function, and Genetics 17:363-374, 1993), two additional ankyrin repeats were identified in *NPR1*; these are shown in Fig. 6B.

In addition, using the MacVector program, a 17 amino acid motif of G-protein coupled receptors (MKGTCEFIVTSLEPDRL, Fig. 5, SEQ ID NO:21) has been found in the  
5 *NPR1* protein (*Science* 244:569-572, 1989).

#### The NPR1-determined Resistance is Dosage Dependent

The ability of NPR-1 to confer disease resistance was evaluated in transgenic plants as follows. The NPR1 cDNA sequence (Fig. 5; SEQ ID NO:2) driven by the constitutive  
10 CaMV 35S promoter was transformed into *Arabidopsis* ecotype Columbia according to standard methods. In the resulting T<sub>3</sub> lines homozygous for the 35S-NPR1 transgene, the  
1: expression of the NPR1-regulated PR-1 gene, NPR1 mRNA, and NPR1 protein were measured to identify those lines exhibiting high (Co1NPR1H), medium (Co1NPR1M), and  
2: low (Co1NPR1L) levels of NPR1 expression. Table 1 shows the results of evaluating the  
3: relative levels of PR-1, NPR1 mRNA, and NPR1 protein concentrations.  
15



**Table 1**  
**Characterization of 35S-NPR1 Transgenic Lines**

5	Genotype	PR-1	NPR1	NPR1
		(INA) <sup>a</sup>	(mRNA) <sup>b</sup>	(Protein) <sup>c</sup>
	Col	1.00	1.00	1.00
	Col-L1	0.41	6.92	0.04
10	Col-L2	0.54	6.90	<0.04
	Col-M1	1.73	9.20	1.40
15	Col-M2	1.80	9.50	1.40
	Col-H1	2.60	17.80	1.60
20	Col-H2	2.74	27.90	3.00

<sup>a</sup> The relative levels of PR-1 were measured by an RNA blot analysis in the 35S-NPR1 transgenic lines grown on plates containing 0.1 mM INA.

<sup>b</sup> The relative levels of NPR1 mRNA were measured by a polyA+RNA blot.

<sup>c</sup> The relative NPR1 protein concentrations were measured by ELISA using NPR1 polyclonal antibodies.

From these experiments, two lines of transformants were identified that had significantly lower NPR1 protein levels (but not mRNA levels) than the wild-type parent. This, however, was not unexpected because overexpression of a transgene in plants often leads to co-suppression of the transgene as well as the corresponding endogenous gene (Baulcombe, *The Plant Cell*, 8:1833, 1996).

The high-, medium-, and low-expressing 35S-NPR1 transgenic lines were next subjected to infection by the bacterial pathogen *Pseudomonas syringae* pv *maculicola* ES4326 and the fungal pathogen *Peronospora parasitica* NOCO2 according to standard methods. The results of these experiments are shown in Figs. 8A and 8B, respectively. In the absence of SAR induction, the high- and the medium-expressing 35S-NPR1 transgenic lines showed significantly increased resistance to both bacterial and fungal pathogens while the low-expressing transgenic lines displayed reduced tolerance to the pathogens as compared

to the wild-type. Together, these results showed that NPR1 was a positive regulator of SAR, and that the NPR1-determined resistance was dosage dependent; overexpression of the NPR1 protein enhanced resistance whereas underexpression led to reduced tolerance to infection.

#### NPR1 is Translocated to the Nucleus Upon SA Induction

5           To elucidate the induction mechanism and the molecular function of the protein, the subcellular localization of NPR1 was determined by using standard reporter gene fusion construct analysis. The green fluorescent protein (GFP) gene was fused to the carboxyl end of the NPR1 cDNA driven by the constitutive CaMV 35S promoter, and the 35S-NPR1-GFP construct was used to transform *npr1* mutants, *npr1-1* and *npr1-2*, according to standard  
10       methods. In the resulting transgenic lines, the NPR1-GFP transgene was found to complement all the *npr1* mutant phenotypes; namely, the lack of SA- or INA-induced PR gene expression, the reduced tolerance to exogenous SA, and the lack of SA- or INA-induced resistance to pathogens (Figs. 9A-9C). Transgenic lines expressing the GFP alone (designated 35S-mGFP), exhibited no complementing activity (Fig. 9B). In addition, the  
15       presence of the NPR-GFP transgene was found to restore both inducible BGL-GUS expression and resistance to *P. parasitica* as shown in Figs. 9A and 9C, respectively. These experiments therefore showed that the NPR1-GFP was biologically active and that the subcellular localization of NPR1-GFP should reflect that of the endogenous NPR1 protein.

          To examine the subcellular localization of the NPR1 protein, the 35S-NPR1-GFP and  
20       35S-mGFP transgenic lines were grown in MS medium in the presence or absence of the SAR-inducing chemicals SA or INA. Eleven-day-old seedlings were subsequently examined using confocal microscopy to detect localization of NPR1-GFP and mGFP. As shown in Fig. 10, the 35S-NPR1-GFP seedlings grown on MS showed low levels of GFP throughout the mesophyll cells and strong GFP fluorescence in the nuclei of the guard cells. Upon induction  
25       by SA or INA, NPR1-GFP was detected exclusively in the nuclei of both the mesophyll cells and the guard cells. In the 35S-mGFP transformants, green fluorescence was detected in the cytoplasm as well as in the nuclei, and SA and INA treatments had no effect on the localization of the protein. These results indicated that NPR1 was localized in the cytoplasm in the mesophyll cells, and that upon induction the NPR1 protein was transported into the  
30       nucleus resulting in PR1 gene expression and resistance. In the guard cells, the NPR1 protein

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was localized in the nuclei even without an SAR induction, an intriguing observation because constitutive activation of defense mechanisms in these cells may be necessary to fend off microbial pathogens from gaining entry into the plant through stomata. Since mGFP alone showed no induced nuclear translocation, the nuclear transport of the NPR1-GFP fusion must be directed by a signal in NPR1. Consistent with this, the following two potential nuclear localization sequences (NLS's) were found in NPR1:

252 RRKELGLEVPKVKK 265 (SEQ ID NO:22); and

541 KKQRYMEIQETLKK 554 (SEQ ID NO:23).

Significantly, nuclear translocation in tissues infected by the virulent pathogen *Psm* ES4326 was also observed (Fig. 11A). This pattern of induction was also observed to coincide with the pattern of PR gene expression observed in plants after infection (Fig. 11B).

#### Characterization of *npr* Mutations

To further characterize the *NPR1* gene, the mutations in *npr1-1*, *npr1-2*, *npr1-3*, and *npr1-4* were identified by DNA sequencing. The mutant *npr1-4* is a new *npr1* allele that was identified in the Col-0 (*BGL2-GUS*) background based on its enhanced susceptibility to *Psm* ES4326. Each mutant allele was found to contain a single base-pair change. The *npr1-1*, *npr1-2*, *npr1-3*, and *npr1-4* alleles respectively altered the highly conserved histidine (residue 334) in the third ankyrin-repeat consensus to a tyrosine, changed a cysteine (residue 150) to a tyrosine, introduced a nonsense codon (residue 400) that should result in a truncated protein lacking 194 amino acids of the C-terminal end of the protein, and destroyed the acceptor site of the third intron junction. All of these point mutations are GC to AT transitions, consistent with the mode of action of the mutagen, ethyl-methanesulfonate (EMS), used for the generation of these mutations.

#### Genetic Analysis of the Plant Defense Response Using *Arabidopsis thaliana*

Although biochemical studies have played an important role in elucidating the general features of the plant defense response, the complexity of the defense response limits the utility of biochemical analysis in determining the importance of particular defense responses or enzymes in conferring resistance to pathogens. Isolation of plant defense-response mutants not only helps elucidate the roles of known pathogen-induced responses in

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combating particular pathogens, but also facilitates the identification of plant defense mechanisms not already correlated with a known biochemical or molecular genetic response. With the development of well-characterized hostpathogen systems involving the model plant *Arabidopsis thaliana* as the host as described herein, comprehensive genetic analysis of acquired resistance responses is made possible.

All of the major features of the plant defense response that have been observed in crop plants have also been observed in *Arabidopsis*-pathogen interactions. For example, several resistance gene-*avr* gene interactions have been identified for both bacterial and fungal pathogens of *Arabidopsis* (Bisgrove et al., *Plant Cell* 6:927-933, 1994; Holub et al., *Mol. Plant-Microbe Interact.* 7:223-239, 1994; Kunkel et al., *Plant Cell* 5:865-875, 1993; Yu et al., *Mol. Plant-Microbe Interact.* 6:434-443, 1993). Moreover, all of the important features of SAR have been observed in *Arabidopsis* (Uknes et al., *Plant Cell* 4:645-656, 1992; Uknes et al., *Mol. Plant-Microbe Interact.* 6:692-698, 1993). Importantly, the power of *Arabidopsis* genetic analysis has recently been used to help identify a variety of components of the *Arabidopsis* defense response to pathogen attack (Bent et al., *Science* 265:1856-1860, 1994; Bowling et al., *Plant Cell* 6:1845-1857, 1994; Cao et al., *Plant Cell* 6:1583-1592, 1994; Century et al., *Proc. Natl. Acad. Sci. USA* 92:6597-6601, 1995; Delaney et al., *Proc. Natl. Acad. Sci. USA* 92:6602-6606, 1995; Dietrich et al., *Cell* 77:565-577, 1994; Glazebrook and Ausubel, *Proc. Natl. Acad. Sci. USA* 91:8955-8959, 1994; Glazebrook et al., *Genetics* 143:973-982, 1996; Grant et al., *Science* 269:843-846, 1995; Greenberg and Ausubel, *Plant J.* 4:327-341, 1993; Greenberg et al., *Plant J.* 4:327-341, 1994; Mindrinos et al., *Cell* 78:1089-1099, 1994). Thus, the results described herein provide the basis for identifying genes that are involved in acquired disease resistance throughout the plant kingdom and are not limited to *Arabidopsis*.

#### Isolation of Solanaceous AR Genes

Using the *Arabidopsis NPR1* cDNA sequence shown in Fig. 5 (SEQ ID NO:2), the isolation of AR homologs that are found in solanaceous plants (e.g., potato, eggplant, tomato, tobacco, petunia, and pepper) is readily accomplished using standard techniques.

For example, a *Nicotiana glutinosa* cDNA library was screened for the presence of an *NPR1* homolog. The library was constructed in the lambda ZAP II vector from poly

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(A+)RNA isolated from *Nicotiana glutinosa* plants infected with tobacco mosaic virus (TMV) (Whitham et al., *Cell* 78: 1101-1115, 1994). Bacteriophage were plated on NZY media using XL-1 Blue host cells. Approximately  $10^6$  plaques were screened by transferring the phage DNA onto positively charged nylon membrane (GeneScreen; DuPont-New England Nuclear) and probing with a random primed  $^{32}\text{P}$  labeled probe that was prepared using the full-length *Arabidopsis NPR1* cDNA as the template. Hybridization was performed at  $37^\circ\text{C}$  in 40% formamide, 5X SSC, 5X Denhardt, 1% SDS, and 10% dextran sulfate. The filters were washed in 2X SSC for fifteen minutes at room temperature and 2X SSC, 1% SDS for thirty minutes at  $37^\circ\text{C}$ .

Two hybridizing clones were identified and purified. The pBluescript plasmids were excised using XL-1 Blue host cells and R408 helper phage. Restriction enzyme analysis indicated that the two positive clones contained inserts of approximately 3600 bp and 2100 bp. Restriction digests and sequence analysis indicated that the 3600 bp insert represented two independent cDNAs of 2100 bp and 1500 bp and that the two independently isolated 2100 bp cDNAs were identical. Both strands of the 2100 bp cDNA were sequenced using  $^{35}\text{S}$ -dATP and the Sequenase sequencing kit (U.S. Biochemicals, Cleveland, OH). The nucleotide and amino acid sequences encoding the *Nicotiana glutinosa NPR1* homolog are shown in Fig. 7A (SEQ ID NO:13) and Fig. 7B (SEQ ID NO:14), respectively.

#### Isolation of Other Acquired Resistance Genes

Any plant cell can serve as the nucleic acid source for the molecular cloning of an AR gene. Isolation of an AR gene involves the isolation of those DNA sequences which encode a protein exhibiting AR-associated structures, properties, or activities, for example, an ankyrin-repeat motif and the ability to induce gene expression of PR proteins that limit pathogen infection. Based on the AR genes and polypeptides described herein, the isolation of additional plant AR coding sequences is made possible using standard strategies and techniques that are well known in the art.

In one particular example, the AR sequences described herein may be used, together with conventional screening methods of nucleic acid hybridization screening. Such hybridization techniques and screening procedures are well known to those skilled in the art and are described, for example, in Benton and Davis, *Science* 196:180, 1977; Grunstein and

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Hogness, *Proc. Natl. Acad. Sci., USA* 72:3961, 1975; Ausubel et al. (*supra*); Berger and Kimmel (*supra*); and Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, New York. In one particular example, all or part of the *NPRI* cDNA (described herein) may be used as a probe to screen a recombinant plant DNA library for genes having sequence identity to the AR gene. Hybridizing sequences are detected by plaque or colony hybridization according to the methods described below.

Alternatively, using all or a portion of the amino acid sequence of the AR polypeptide, one may readily design AR-specific oligonucleotide probes, including AR degenerate oligonucleotide probes (i.e., a mixture of all possible coding sequences for a given amino acid sequence). These oligonucleotides may be based upon the sequence of either DNA strand and any appropriate portion of the AR sequence (Figs. 4 and 5, 7A, and 7B SEQ ID NOS:1, 2, 3, 13, and 14, respectively). General methods for designing and preparing such probes are provided, for example, in Ausubel et al., 1996, *Current Protocols in Molecular Biology*, Wiley Interscience, New York, and Berger and Kimmel, *Guide to Molecular Cloning Techniques*, 1987, Academic Press, New York. These oligonucleotides are useful for AR gene isolation, either through their use as probes capable of hybridizing to AR complementary sequences or as primers for various amplification techniques, for example, polymerase chain reaction (PCR) cloning strategies. If desired, a combination of different oligonucleotide probes may be used for the screening of a recombinant DNA library. The oligonucleotides may be detectably-labeled using methods known in the art and used to probe filter replicas from a recombinant DNA library. Recombinant DNA libraries are prepared according to methods well known in the art, for example, as described in Ausubel et al. (*supra*), or they may be obtained from commercial sources.

In one particular example of this approach, related AR sequences having greater than 80% identity are detected or isolated using high stringency conditions. High stringency conditions may include hybridization at about 42°C and about 50% formamide, 0.1 mg/mL sheared salmon sperm DNA, 1% SDS, 2X SSC, 10% Dextran sulfate, a first wash at about 65°C, about 2X SSC, and 1% SDS, followed by a second wash at about 65°C and about 0.1X SSC. Alternatively, high stringency conditions may include hybridization at about 42°C and about 50% formamide, 0.1 mg/mL sheared salmon sperm DNA, 0.5% SDS, 5X SSPE, 1X

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Denhardt's, followed by two washes at room temperature and 2X SSC, 0.1% SDS, and two washes at between 55-60°C and 0.2X SSC, 0.1% SDS.

In another approach, low stringency hybridization conditions for detecting AR genes having about 40% or greater sequence identity to the AR genes described herein include, for example, hybridization at about 42°C and 0.1 mg/mL sheared salmon sperm DNA, 1% SDS, 2X SSC, and 10% Dextran sulfate (in the absence of formamide), and a wash at about 37°C and 6X SSC, about 1% SDS. Alternatively, the low stringency hybridization may be carried out at about 42°C and 40% formamide, 0.1 mg/mL sheared salmon sperm DNA, 0.5% SDS, 5X SSPE, 1X Denhardt's, followed by two washes at room temperature and 2X SSC, 0.1% SDS and two washes at room temperature and 0.5X SSC, 0.1% SDS. These stringency conditions are exemplary; other appropriate conditions may be determined by those skilled in the art.

If desired, RNA gel blot analysis of total or poly(A+) RNAs isolated from any plant (e.g., those crop plants described herein) may be used to determine the presence or absence of an AR transcript using conventional methods. As an example, a Northern blot of potato RNA was prepared according to standard methods and probed with a 1.96-kb *NPR1* *Hind*III fragment in a hybridization solution containing 50% formamide, 5X SSC, 2.5X Denhardt's solution, and 300 µg/mL salmon sperm DNA at 37°C. Following overnight hybridization, the blot was washed two times for ten minutes each in a solution containing 1X SSC, 0.2% SDS at 37°C. An autoradiogram of the blot demonstrated the presence an *NPR1*-hybridizing RNA in the potato RNA sample, indicating that this solanaceous crop plant encoded an acquired resistance gene. These results further indicate that AR genes are not restricted to the crucifer *Arabidopsis*. Isolation of this hybridizing transcript is performed using standard cDNA cloning techniques.

As discussed above, AR oligonucleotides may also be used as primers in amplification cloning strategies, for example, using PCR. PCR methods are well known in the art and are described, for example, in *PCR Technology*, Erlich, ed., Stockton Press, London, 1989; *PCR Protocols: A Guide to Methods and Applications*, Innis et al., eds., Academic Press, Inc., New York, 1990; and Ausubel et al. (*supra*). Primers are optionally designed to allow cloning of the amplified product into a suitable vector, for example, by

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including appropriate restriction sites at the 5' and 3' ends of the amplified fragment (as described herein). If desired, AR sequences may be isolated using the PCR "RACE" technique, or Rapid Amplification of cDNA Ends (see, e.g., Innis et al. (*supra*)). By this method, oligonucleotide primers based on an AR sequence are oriented in the 3' and 5' directions and are used to generate overlapping PCR fragments. These overlapping 3'- and 5'-end RACE products are combined to produce an intact full-length cDNA. This method is described in Innis et al. (*supra*); and Frohman et al., *Proc. Natl. Acad. Sci. USA* 85:8998, 1988. Exemplary oligonucleotide primers useful for amplifying AR gene sequences include, without limitation:

- 10       A.     AA(A/G)GA(A/G)GA(T/C)CA(T/C)ACNAA (SEQ ID NO:24);
- B.     TA(T/C)TG(T/C)AA(T/C)GTNAA(A/G)AC (SEQ ID NO:25);
- C.     GCCATNGTNGC(T/C)TG(T/C)TT (SEQ ID NO:26);
- D.     AA(A/G)GTNAA(A/G)AA(A/G)CA(C/T)GT (SEQ ID NO:27);
- E.     (A/G)AA(C/T)TC(A/G)CANGTNCC(C/T)TTCAT (SEQ ID NO:28).

- 15   For each of the above sequences, N is A, T, G or C.

Alternatively, any plant cDNA or cDNA expression library may be screened by functional complementation of an *npr* mutant (for example, the *npr1* mutant described herein) according to standard methods described herein.

- 20       Confirmation of a sequence's relatedness to the AR polypeptide family may be accomplished by a variety of conventional methods including, but not limited to, functional complementation assays and sequence comparison of the gene and its expressed product. In addition, the activity of the gene product may be evaluated according to any of the techniques described herein, for example, the functional or immunological properties of its encoded product.

- 25       Once an AR sequence is identified, it is cloned according to standard methods and used for the construction of plant expression vectors as described below.

#### AR Polypeptide Expression

- 30       AR polypeptides may be expressed and produced by transformation of a suitable host cell with all or part of an AR cDNA (for example, the cDNA described above) in a suitable expression vehicle or with a plasmid construct engineered for increasing the expression of an



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AR polypeptide (*supra*) *in vivo*.

Those skilled in the field of molecular biology will understand that any of a wide variety of expression systems may be used to provide the recombinant protein. The precise host cell used is not critical to the invention. The AR protein may be produced in a

5 prokaryotic host, for example, *E. coli*, or in a eukaryotic host, for example, *Saccharomyces cerevisiae*, mammalian cells (for example, COS 1 or NIH 3T3 cells), or any of a number of plant cells or whole plant including, without limitation, algae, tree species, ornamental species, temperate fruit species, tropical fruit species, vegetable species, legume species, crucifer species, monocots, dicots, or in any plant of commercial or agricultural significance.

10 Particular examples of suitable plant hosts include, but are not limited to, conifers, petunia, tomato, potato, pepper, tobacco, *Arabidopsis*, lettuce, sunflower, oilseed rape, flax, cotton, sugarbeet, celery, soybean, alfalfa, *Medicago*, lotus, *Vigna*, cucumber, carrot, eggplant, cauliflower, horseradish, morning glory, poplar, walnut, apple, grape, asparagus, cassava, rice, maize, millet, onion, barley, orchard grass, oat, rye, and wheat.

15 Such cells are available from a wide range of sources including the American Type Culture Collection (Rockland, MD); or from any of a number seed companies, for example, W. Atlee Burpee Seed Co. (Warminster, PA), Park Seed Co. (Greenwood, SC), Johnny Seed Co. (Albion, ME), or Northrup King Seeds (Harstville, SC). Descriptions and sources of useful host cells are also found in Vasil I.K., *Cell Culture and Somatic Cell Genetics of*

20 *Plants*, Vol I, II, III Laboratory Procedures and Their Applications Academic Press, New York, 1984; Dixon, R.A., *Plant Cell Culture-A Practical Approach*, IRL Press, Oxford University, 1985; Green et al., *Plant Tissue and Cell Culture*, Academic Press, New York, 1987; and Gasser and Fraley, *Science* 244:1293, 1989.

For prokaryotic expression, DNA encoding an AR polypeptide is carried on a vector

25 operably linked to control signals capable of effecting expression in the prokaryotic host. If desired, the coding sequence may contain, at its 5' end, a sequence encoding any of the known signal sequences capable of effecting secretion of the expressed protein into the periplasmic space of the host cell, thereby facilitating recovery of the protein and subsequent purification. Prokaryotes most frequently used are various strains of *E. coli*; however, other

30 microbial strains may also be used. Plasmid vectors are used which contain replication

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origins, selectable markers, and control sequences derived from a species compatible with the microbial host. Examples of such vectors are found in Pouwels et al. (*supra*) or Ausubel et al. (*supra*). Commonly used prokaryotic control sequences (also referred to as "regulatory elements") are defined herein to include promoters for transcription initiation, optionally with an operator, along with ribosome binding site sequences. Promoters commonly used to direct protein expression include the beta-lactamase (penicillinase), the lactose (lac) (Chang et al., *Nature* 198:1056, 1977), the tryptophan (Trp) (Goeddel et al., *Nucl. Acids Res.* 8:4057, 1980), and the *tac* promoter systems, as well as the lambda-derived P<sub>L</sub> promoter and N-gene ribosome binding site (Simatake et al., *Nature* 292:128, 1981).

One particular bacterial expression system for AR polypeptide production is the *E. coli* pET expression system (Novagen, Inc., Madison, WI). According to this expression system, DNA encoding an AR polypeptide is inserted into a pET vector in an orientation designed to allow expression. Since the AR gene is under the control of the T7 regulatory signals, expression of AR is induced by inducing the expression of T7 RNA polymerase in the host cell. This is typically achieved using host strains which express T7 RNA polymerase in response to IPTG induction. Once produced, recombinant AR polypeptide is then isolated according to standard methods known in the art, for example, those described herein.

Another bacterial expression system for AR polypeptide production is the pGEX expression system (Pharmacia). This system employs a GST gene fusion system which is designed for high-level expression of genes or gene fragments as fusion proteins with rapid purification and recovery of functional gene products. The protein of interest is fused to the carboxyl terminus of the glutathione S-transferase protein from *Schistosoma japonicum* and is readily purified from bacterial lysates by affinity chromatography using Glutathione Sepharose 4B. Fusion proteins can be recovered under mild conditions by elution with glutathione. Cleavage of the glutathione S-transferase domain from the fusion protein is facilitated by the presence of recognition sites for site-specific proteases upstream of this domain. For example, proteins expressed in pGEX-2T plasmids may be cleaved with thrombin; those expressed in pGEX-3X may be cleaved with factor Xa.

For eukaryotic expression, the method of transformation or transfection and the choice of vehicle for expression of the AR polypeptide will depend on the host system

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selected. Transformation and transfection methods are described, e.g., in Ausubel et al. (*supra*); Weissbach and Weissbach, *Methods for Plant Molecular Biology*, Academic Press, 1989; Gelvin et al., *Plant Molecular Biology Manual*, Kluwer Academic Publishers, 1990; Kindle, K., *Proc. Natl. Acad. Sci., U.S.A.* 87:1228, 1990; Potrykus, I., *Annu. Rev. Plant Physiol. Plant Mol. Biology* 42:205, 1991; and BioRad (Hercules, CA) Technical Bulletin #1687 (Biolistic Particle Delivery Systems). Expression vehicles may be chosen from those provided, e.g., in *Cloning Vectors: A Laboratory Manual* (P.H. Pouwels et al., 1985, Supp. 1987); Gasser and Fraley (*supra*); Clontech Molecular Biology Catalog (Catalog 1992/93 Tools for the Molecular Biologist, Palo Alto, CA); and the references cited above. Other expression constructs are described by Fraley et al. (U.S. Pat. No. 5,352,605).

#### Construction of Plant Transgenes

Most preferably, an AR polypeptide is produced by a stably-transfected plant cell line, a transiently-transfected plant cell line, or by a transgenic plant. A number of vectors suitable for stable or extrachromosomal transfection of plant cells or for the establishment of transgenic plants are available to the public; such vectors are described in Pouwels et al. (*supra*), Weissbach and Weissbach (*supra*), and Gelvin et al. (*supra*). Methods for constructing such cell lines are described in, e.g., Weissbach and Weissbach (*supra*), and Gelvin et al. (*supra*).

Typically, plant expression vectors include (1) a cloned plant gene under the transcriptional control of 5' and 3' regulatory sequences and (2) a dominant selectable marker. Such plant expression vectors may also contain, if desired, a promoter regulatory region (for example, one conferring inducible or constitutive, pathogen- or wound-induced, environmentally- or developmentally-regulated, or cell- or tissue-specific expression), a transcription initiation start site, a ribosome binding site, an RNA processing signal, a transcription termination site, and/or a polyadenylation signal.

Once the desired AR nucleic acid sequence is obtained as described above, it may be manipulated in a variety of ways known in the art. For example, where the sequence involves non-coding flanking regions, the flanking regions may be subjected to mutagenesis.

The AR DNA sequence of the invention may, if desired, be combined with other DNA sequences in a variety of ways. The AR DNA sequence of the invention may be

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employed with all or part of the gene sequences normally associated with the AR protein. In its component parts, a DNA sequence encoding an AR protein is combined in a DNA construct having a transcription initiation control region capable of promoting transcription and translation in a host cell.

5           In general, the constructs will involve regulatory regions functional in plants which provide for modified production of AR protein as discussed herein. The open reading frame coding for the AR protein or functional fragment thereof will be joined at its 5' end to a transcription initiation regulatory region such as the sequence naturally found in the 5' upstream region of the AR structural gene. Numerous other transcription initiation regions  
10           are available which provide for constitutive or inducible regulation.

For applications where developmental, cell, tissue, hormonal, or environmental expression is desired, appropriate 5' upstream non-coding regions are obtained from other genes, for example, from genes regulated during meristem development, seed development, embryo development, or leaf development.

15           Regulatory transcript termination regions may also be provided in DNA constructs of this invention as well. Transcript termination regions may be provided by the DNA sequence encoding the AR protein or any convenient transcription termination region derived from a different gene source. The transcript termination region will contain preferably at least 1-3 kb of sequence 3' to the structural gene from which the termination region is derived. Plant  
20           expression constructs having AR as the DNA sequence of interest for expression (in either the sense or antisense orientation) may be employed with a wide variety of plant life, particularly plant life involved in the production of storage reserves (for example, those involving carbon and nitrogen metabolism). Such genetically-engineered plants are useful for a variety of industrial and agricultural applications as discussed infra. Importantly, this  
25           invention is applicable to dicotyledons and monocotyledons, and will be readily applicable to any new or improved transformation or regeneration method.

The expression constructs include at least one promoter operably linked to at least one AR gene. An example of a useful plant promoter according to the invention is a caulimovirus promoter, for example, a cauliflower mosaic virus (CaMV) promoter. These promoters  
30           confer high levels of expression in most plant tissues, and the activity of these promoters is

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not dependent on virally encoded proteins. CaMV is a source for both the 35S and 19S promoters. Examples of plant expression constructs using these promoters are found in Fraley et al., U.S. Pat. No. 5,352,605. In most tissues of transgenic plants, the CaMV 35S promoter is a strong promoter (see, e.g., Odell et al., *Nature* 313:810, 1985). The CaMV promoter is also highly active in monocots (see, e.g., Dekeyser et al., *Plant Cell* 2:591, 1990; Terada and Shimamoto, *Mol. Gen. Genet.* 220:389, 1990). Moreover, activity of this promoter can be further increased (i.e., between 2-10 fold) by duplication of the CaMV 35S promoter (see e.g., Kay et al., *Science* 236:1299, 1987; Ow et al., *Proc. Natl. Acad. Sci. U.S.A.* 84:4870, 1987; and Fang et al., *Plant Cell* 1:141, 1989, and McPherson and Kay, U.S. Pat. No. 5,378,142).

Other useful plant promoters include, without limitation, the nopaline synthase (NOS) promoter (An et al., *Plant Physiol.* 88:547, 1988 and Rodgers and Fraley, U.S. Pat. No. 5,034,322), the octopine synthase promoter (Fromm et al., *Plant Cell* 1:977, 1989), figwort mosaic virus (FMV) promoter (Rodgers, U.S. Pat. No. 5,378,619), and the rice actin promoter (Wu and McElroy, W091/09948).

Exemplary monocot promoters include, without limitation, commelina yellow mottle virus promoter, sugar cane badna virus promoter, rice tungro bacilliform virus promoter, maize streak virus element, and wheat dwarf virus promoter.

For certain applications, it may be desirable to produce the AR gene product in an appropriate tissue, at an appropriate level, or at an appropriate developmental time. For this purpose, there are an assortment of gene promoters, each with its own distinct characteristics embodied in its regulatory sequences, shown to be regulated in response to inducible signals such as the environment, hormones, and/or developmental cues. These include, without limitation, gene promoters that are responsible for heat-regulated gene expression (see, e.g., Callis et al., *Plant Physiol.* 88:965, 1988; Takahashi and Komeda, *Mol. Gen. Genet.* 219:365, 1989; and Takahashi et al. *Plant J.* 2:751, 1992), light-regulated gene expression (e.g., the pea *rbcS-3A* described by Kuhlemeier et al., *Plant Cell* 1:471, 1989; the maize *rbcS* promoter described by Schäffner and Sheen, *Plant Cell* 3:997, 1991; the chlorophyll a/b-binding protein gene found in pea described by Simpson et al., *EMBO J.* 4:2723, 1985; the Arabidopsis promoter; or the rice rbs promoter), hormone-regulated gene expression (for example, the

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abscisic acid (ABA) responsive sequences from the *Em* gene of wheat described by Marcotte et al., *Plant Cell* 1:969, 1989; the ABA-inducible HVA1 and HVA22, and rd29A promoters described for barley and *Arabidopsis* by Straub et al., *Plant Cell* 6:617, 1994 and Shen et al., *Plant Cell* 7:295, 1995; and wound-induced gene expression (for example, of *wun1* described  
5 by Siebertz et al., *Plant Cell* 1:961, 1989), organ-specific gene expression (for example, of the tuber-specific storage protein gene described by Roshal et al., *EMBO J.* 6:1155, 1987; the 23-kDa zein gene from maize described by Schernthaner et al., *EMBO J.* 7:1249, 1988; or the French bean  $\beta$ -phaseolin gene described by Bustos et al., *Plant Cell* 1:839, 1989), or pathogen-inducible promoters (for example, PR-1, prp-1, or  $\beta$ -1,3 glucanase promoters, the  
10 fungal-inducible wirla promoter of wheat, and the nematode-inducible promoters, TobRB7-5A and Hmg-1, of tobacco and parsley, respectively).

Plant expression vectors may also optionally include RNA processing signals, e.g., introns, which have been shown to be important for efficient RNA synthesis and accumulation (Callis et al., *Genes and Dev.* 1:1183, 1987). The location of the RNA splice  
15 sequences can dramatically influence the level of transgene expression in plants. In view of this fact, an intron may be positioned upstream or downstream of an AR polypeptide-encoding sequence in the transgene to modulate levels of gene expression.

In addition to the aforementioned 5' regulatory control sequences, the expression vectors may also include regulatory control regions which are generally present in the 3'  
20 regions of plant genes (Thornburg et al., *Proc. Natl. Acad. Sci. U.S.A.* 84:744, 1987; An et al., *Plant Cell* 1:115, 1989). For example, the 3' terminator region may be included in the expression vector to increase stability of the mRNA. One such terminator region may be derived from the PI-II terminator region of potato. In addition, other commonly used terminators are derived from the octopine or nopaline synthase signals.

25 The plant expression vector also typically contains a dominant selectable marker gene used to identify those cells that have become transformed. Useful selectable genes for plant systems include genes encoding antibiotic resistance genes, for example, those encoding resistance to hygromycin, kanamycin, bleomycin, G418, streptomycin, or spectinomycin. Genes required for photosynthesis may also be used as selectable markers in photosynthetic-  
30 deficient strains. Finally, genes encoding herbicide resistance may be used as selectable

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markers; useful herbicide resistance genes include the *bar* gene encoding the enzyme phosphinothricin acetyltransferase and conferring resistance to the broad spectrum herbicide Basta® (Hoechst AG, Frankfurt, Germany).

Efficient use of selectable markers is facilitated by a determination of the susceptibility of a plant cell to a particular selectable agent and a determination of the concentration of this agent which effectively kills most, if not all, of the transformed cells. Some useful concentrations of antibiotics for tobacco transformation include, e.g., 75-100 µg/mL (kanamycin), 20-50 µg/mL (hygromycin), or 5-10 µg/mL (bleomycin). A useful strategy for selection of transformants for herbicide resistance is described, e.g., by Vasil et al., *supra*.

In addition, if desired, the plant expression construct may contain a modified or fully-synthetic structural AR coding sequence which has been changed to enhance the performance of the gene in plants. Methods for constructing such a modified or synthetic gene are described in Fischhoff and Perlak, U.S. Pat. No. 5,500,365.

It should be readily apparent to one skilled in the art of molecular biology, especially in the field of plant molecular biology, that the level of gene expression is dependent, not only on the combination of promoters, RNA processing signals, and terminator elements, but also on how these elements are used to increase the levels of selectable marker gene expression.

#### Plant Transformation

Upon construction of the plant expression vector, several standard methods are available for introduction of the vector into a plant host, thereby generating a transgenic plant. These methods include (1) *Agrobacterium*-mediated transformation (*A. tumefaciens* or *A. rhizogenes*) (see, e.g., Lichtenstein and Fuller In: *Genetic Engineering*, vol 6, PWJ Rigby, ed, London, Academic Press, 1987; and Lichtenstein, C.P., and Draper, J., In: *DNA Cloning*, Vol II, D.M. Glover, ed, Oxford, IRI Press, 1985)), (2) the particle delivery system (see, e.g., Gordon-Kamm et al., *Plant Cell* 2:603 (1990); or BioRad Technical Bulletin 1687, *supra*), (3) microinjection protocols (see, e.g., Green et al., *supra*), (4) polyethylene glycol (PEG) procedures (see, e.g., Draper et al., *Plant Cell Physiol.* 23:451, 1982; or e.g., Zhang and Wu, *Theor. Appl. Genet.* 76:835, 1988), (5) liposome-mediated DNA uptake (see, e.g., Freeman et

al., *Plant Cell Physiol.* 25:1353, 1984), (6) electroporation protocols (see, e.g., Gelvin et al., *supra*; Dekeyser et al., *supra*; Fromm et al., *Nature* 319:791, 1986; Sheen *Plant Cell* 2:1027, 1990; or Jang and Sheen *Plant Cell* 6:1665, 1994), and (7) the vortexing method (see, e.g., Kindle *supra*). The method of transformation is not critical to the invention. Any method  
5 which provides for efficient transformation may be employed. As newer methods are available to transform crops or other host cells, they may be directly applied. Suitable plants for use in the practice of the invention include, but are not limited to, sugar cane, wheat, rice, maize, sugar beet, potato, barley, manioc, sweet potato, soybean, sorghum, cassava, banana, grape, oats, tomato, millet, coconut, orange, rye, cabbage, apple, watermelon, canola, cotton,  
10 carrot, garlic, onion, pepper, strawberry, yam, peanut, onion, bean, pea, mango, citrus plants, walnuts, and sunflower.

The following is an example outlining one particular technique, an *Agrobacterium*-mediated plant transformation. By this technique, the general process for manipulating genes to be transferred into the genome of plant cells is carried out in two phases. First, cloning and  
15 DNA modification steps are carried out in *E. coli*, and the plasmid containing the gene construct of interest is transferred by conjugation or electroporation into *Agrobacterium*. Second, the resulting *Agrobacterium* strain is used to transform plant cells. Thus, for the generalized plant expression vector, the plasmid contains an origin of replication that allows it to replicate in *Agrobacterium* and a high copy number origin of replication functional in *E.*  
20 *coli*. This permits facile production and testing of transgenes in *E. coli* prior to transfer to *Agrobacterium* for subsequent introduction into plants. Resistance genes can be carried on the vector, one for selection in bacteria, for example, streptomycin, and another that will function in plants, for example, a gene encoding kanamycin resistance or herbicide resistance. Also present on the vector are restriction endonuclease sites for the addition of one or more  
25 transgenes and directional T-DNA border sequences which, when recognized by the transfer functions of *Agrobacterium*, delimit the DNA region that will be transferred to the plant.

In another example, plant cells may be transformed by shooting into the cell tungsten microprojectiles on which cloned DNA is precipitated. In the Biolistic Apparatus (Bio-Rad) used for the shooting, a gunpowder charge (22 caliber Power Piston Tool Charge) or an air-  
30 driven blast drives a plastic macroprojectile through a gun barrel. An aliquot of a suspension



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of tungsten particles on which DNA has been precipitated is placed on the front of the plastic macroprojectile. The latter is fired at an acrylic stopping plate that has a hole through it that is too small for the macroprojectile to pass through. As a result, the plastic macroprojectile smashes against the stopping plate, and the tungsten microprojectiles continue toward their target through the hole in the plate. For the instant invention the target can be any plant cell, tissue, seed, or embryo. The DNA introduced into the cell on the microprojectiles becomes integrated into either the nucleus or the chloroplast.

In general, transfer and expression of transgenes in plant cells are now routine practices to those skilled in the art, and have become major tools to carry out gene expression studies in plants and to produce improved plant varieties of agricultural or commercial interest.

#### Transgenic Plant Regeneration

Plant cells transformed with a plant expression vector can be regenerated, for example, from single cells, callus tissue, or leaf discs according to standard plant tissue culture techniques. It is well known in the art that various cells, tissues, and organs from almost any plant can be successfully cultured to regenerate an entire plant; such techniques are described, e.g., in Vasil *supra*; Green et al., *supra*; Weissbach and Weissbach, *supra*; and Gelvin et al., *supra*.

In one particular example, a cloned AR polypeptide construct under the control of the 35S CaMV promoter and the nopaline synthase terminator and carrying a selectable marker (for example, kanamycin resistance) is transformed into *Agrobacterium*. Transformation of leaf discs (for example, of tobacco or potato leaf discs), with vector-containing *Agrobacterium* is carried out as described by Horsch et al. (*Science* 227:1229, 1985).

Putative transformants are selected after a few weeks (for example, 3 to 5 weeks) on plant tissue culture media containing kanamycin (e.g. 100 µg/mL). Kanamycin-resistant shoots are then placed on plant tissue culture media without hormones for root initiation. Kanamycin-resistant plants are then selected for greenhouse growth. If desired, seeds from self-fertilized transgenic plants can then be sowed in a soil-less medium and grown in a greenhouse.

Kanamycin-resistant progeny are selected by sowing surfaced sterilized seeds on hormone-free kanamycin-containing media. Analysis for the integration of the transgene is

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accomplished by standard techniques (see, for example, Ausubel et al. *supra*; Gelvin et al. *supra*).

Transgenic plants expressing the selectable marker are then screened for transmission of the transgene DNA by standard immunoblot and DNA detection techniques. Each positive  
5 transgenic plant and its transgenic progeny are unique in comparison to other transgenic plants established with the same transgene. Integration of the transgene DNA into the plant genomic DNA is in most cases random, and the site of integration can profoundly affect the levels and the tissue and developmental patterns of transgene expression. Consequently, a number of transgenic lines are usually screened for each transgene to identify and select  
10 plants with the most appropriate expression profiles.

Transgenic lines are evaluated for levels of transgene expression. Expression at the RNA level is determined initially to identify and quantitate expression-positive plants. Standard techniques for RNA analysis are employed and include PCR amplification assays using oligonucleotide primers designed to amplify only transgene RNA templates and  
15 solution hybridization assays using transgene-specific probes (see, e.g., Ausubel et al., *supra*). The RNA-positive plants are then analyzed for protein expression by Western immunoblot analysis using AR specific antibodies (see, e.g., Ausubel et al., *supra*). In addition, *in situ* hybridization and immunocytochemistry according to standard protocols can be done using transgene-specific nucleotide probes and antibodies, respectively, to localize  
20 sites of expression within transgenic tissue.

Ectopic expression of AR genes is useful for the production of transgenic plants having an increased level of resistance to disease-causing pathogens.

In addition, if desired, once the recombinant AR protein is expressed in any cell or in a transgenic plant (for example, as described above), it may be isolated, e.g., using affinity  
25 chromatography. In one example, an anti-AR polypeptide antibody (e.g., produced as described in Ausubel et al., *supra*, or by any standard technique) may be attached to a column and used to isolate the polypeptide. Lysis and fractionation of AR-producing cells prior to affinity chromatography may be performed by standard methods (see, e.g., Ausubel et al., *supra*). Once isolated, the recombinant protein can, if desired, be further purified, for  
30 example, by high performance liquid chromatography (see, e.g., Fisher, *Laboratory*

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*Techniques In Biochemistry And Molecular Biology*, eds., Work and Burdon, Elsevier, 1980).

Polypeptides of the invention, particularly short AR protein fragments, can also be produced by chemical synthesis (e.g., by the methods described in *Solid Phase Peptide Synthesis*, 2nd ed., 1984 The Pierce Chemical Co., Rockford, IL). These general techniques of polypeptide expression and purification can also be used to produce and isolate useful AR fragments or analogs.

#### Ectopic Expression of AR Genes for Engineering Plant Defense Responses to Pathogens

As discussed above, plasmid constructs designed for the expression of AR gene products are useful, for example, for activating plant defense pathways that confer anti-pathogenic properties to a transgenic plant. AR genes that are isolated from a host plant (e.g., *Arabidopsis* or *Nicotiana*) may be engineered for expression in the same plant, a closely related species, or a distantly related plant species. For example, the cruciferous *Arabidopsis NPR1* gene may be engineered for constitutive low level expression and then transformed into an *Arabidopsis* host plant. Alternatively, the *Arabidopsis NPR1* gene may be engineered for expression in other cruciferous plants, such as the Brassicas (for example, broccoli, cabbage, and cauliflower). Similarly, the *NPR1* homolog of *Nicotiana glutinosa* is useful for expression in related solanaceous plants, such as tomato, potato, and pepper. To achieve pathogen resistance, it is important to express an AR protein at an effective level. Evaluation of the level of pathogen protection conferred to a plant by ectopic expression of an AR gene is determined according to conventional methods and assays.

In one working example, constitutive ectopic expression of the *NPR1* gene of *Arabidopsis* (Fig. 5; SEQ ID NO:2) or the *NPR1* homolog of *Nicotiana glutinosa* (Fig. 7A; SEQ ID NO:13) in Russet Burbank potato is used to control *Phytophthora infestans* infection. In one particular example, a plant expression vector is constructed that contains an *NPR1* cDNA sequence expressed under the control of the enhanced CaMV 35S promoter as described by McPherson and Kay (U.S. Patent 5,359,142). This expression vector is then used to transform Russet Burbank according to the methods described in Fischhoff et al. (U.S. Patent 5,500,365). To assess resistance to fungal infection, transformed Russet Burbank and appropriate controls are grown to approximately eight-weeks-old, and leaves (for example, the second or third from the top of the plant) are inoculated with a mycelial

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suspension of *P. infestans*. Plugs of *P. infestans* mycelia are inoculated on each side of the leaf midvein. Plants are subsequently incubated in a growth chamber at 27°C with constant fluorescent light.

Leaves of transformed Russet Burbank and control plants are then evaluated for resistance to *P. infestans* infection according to conventional experimental methods. For this evaluation, the number of lesions per leaf and percentage of leaf area infected are recorded every twenty-four hours for seven days after inoculation. From these data, levels of resistance to *P. infestans* are determined. Transformed potato plants that express an *NPR1* gene having an increased level of resistance to *P. infestans* relative to control plants are taken as being useful in the invention.

Alternatively, to assess resistance at the whole plant level, transformed and control plants are transplanted to potting soil containing an inoculum of *P. infestans*. Plants are then evaluated for symptoms of fungal infection (for example, wilting or decayed leaves) over a period of time lasting from several days to weeks. Again, transformed potato plants expressing the *NPR1* gene having an increased level of resistance to the fungal pathogen, *P. infestans*, relative to control plants are taken as being useful in the invention.

In another working example, expression of the *NPR1* homolog of *Nicotiana glutinosa* in tomato is used to control bacterial infection, for example, to *Pseudomonas syringae*. Specifically, a plant expression vector is constructed that contains the cDNA sequence of the *NPR1* homolog from *Nicotiana glutinosa* (Fig. 7A; SEQ ID NO:13) which is expressed under the control of the enhanced CaMV 35S promoter as described by McPherson and Kay, *supra*. This expression vector is then used to transform tomato plants according to the methods described in Fischhoff et al., *supra*. To assess resistance to bacterial infection, transformed tomato plants and appropriate controls are grown, and their leaves are inoculated with a suspension of *P. syringae* according to standard methods, for example, those described herein. Plants are subsequently incubated in a growth chamber, and the inoculated leaves are subsequently analyzed for signs of disease resistance according to standard methods. For example, the number of chlorotic lesions per leaf and percentage of leaf area infected are recorded and evaluated after inoculation. From a statistical analysis of these data, levels of resistance to *P. syringae* are determined. Transformed tomato plants that express an *NPR1*

homolog of *Nicotiana glutinosa* gene having an increased level of resistance to *P. syringae* relative to control plants are taken as being useful in the invention.

In still another working example, expression of the *NPR1* homolog of rice is used to control fungal diseases, for example, the infection of tissue by *Magnaporthe grisea*, the cause of rice blast. In one particular approach, a plant expression vector is constructed that contains the cDNA sequence of the *rice NPR1* homolog that is constitutively expressed under the control of the rice actin promoter described by Wu et al. (WO 91/09948). This expression vector is then used to transform rice plants according to conventional methods, for example, using the methods described in Hiei et al. (*Plant Journal* 6:271-282, 1994). To assess resistance to fungal infection, transformed rice plants and appropriate controls are grown, and their leaves are inoculated with a mycelial suspension of *M. grisea* according to standard methods. Plants are subsequently incubated in a growth chamber and the inoculated leaves are subsequently analyzed for disease resistance according to standard methods. For example, the number of lesions per leaf and percentage of leaf area infected are recorded and evaluated after inoculation. From a statistical analysis of these data, levels of resistance to *M. grisea* are determined. Transformed rice plants that express a rice *NPR1* homolog having an increased level of resistance to *M. grisea* relative to control plants are taken as being useful in the invention.

#### AR Interacting Polypeptides

The isolation of AR sequences also facilitates the identification of polypeptides which interact with the AR protein. Such polypeptide-encoding sequences are isolated by any standard two hybrid system (see, for example, Fields et al., *Nature* 340:245-246, 1989; Yang et al., *Science* 257:680-682, 1992; Zervos et al., *Cell* 72:223-232, 1993). For example, all or a part of the AR sequence may be fused to a DNA binding domain (such as the GAL4 or LexA DNA binding domain). After establishing that this fusion protein does not itself activate expression of a reporter gene (for example, a lacZ or LEU2 reporter gene) bearing appropriate DNA binding sites, this fusion protein is used as an interaction target. Candidate interacting proteins fused to an activation domain (for example, an acidic activation domain) are then co-expressed with the AR fusion in host cells, and interacting proteins are identified

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by their ability to contact the AR sequence and stimulate reporter gene expression. AR-interacting proteins identified using this screening method provide good candidates for proteins that are involved in the acquired resistance signal transduction pathway.

#### Antibodies

5 AR polypeptides described herein (or immunogenic fragments or analogs) may be used to raise antibodies useful in the invention; such polypeptides may be produced by recombinant or peptide synthetic techniques (see, e.g., *Solid Phase Peptide Synthesis*, 2nd ed., 1984, Pierce Chemical Co., Rockford, IL; Ausubel et al., *supra*). The peptides may be coupled to a carrier protein, such as KLH as described in Ausubel et al, *supra*. The KLH-  
10 peptide is mixed with Freund's adjuvant and injected into guinea pigs, rats, or preferably rabbits. Antibodies may be purified by peptide antigen affinity chromatography.

Monoclonal antibodies may be prepared using the AR polypeptides described above and standard hybridoma technology (see, e.g., Kohler et al., *Nature* 256:495, 1975; Kohler et al., *Eur. J. Immunol.* 6:511, 1976; Kohler et al., *Eur. J. Immunol.* 6:292, 1976; Hammerling et  
15 al., *In Monoclonal Antibodies and T Cell Hybridomas*, Elsevier, NY, 1981; Ausubel et al., *supra*).

Once produced, polyclonal or monoclonal antibodies are tested for specific AR recognition by Western blot or immunoprecipitation analysis (by the methods described in Ausubel et al., *supra*). Antibodies which specifically recognize AR polypeptides are  
20 considered to be useful in the invention; such antibodies may be used, e.g., in an immunoassay to monitor the level of AR polypeptide produced by a plant.

#### Use

The invention described herein is useful for a variety of agricultural and commercial purposes including, but not limited to, improving acquired resistance against plant pathogens,  
25 increasing crop yields, improving crop and ornamental quality, and reducing agricultural production costs. In particular, ectopic expression of an *AR* gene in a plant cell provides acquired resistance to plant pathogens and can be used to protect plants from pathogen infestation that reduces plant productivity and viability.

The invention also provides for broad-spectrum pathogen resistance by facilitating the  
30 natural mechanism of host resistance. For example, AR transgenes can be expressed in plant

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cells at sufficiently high levels to initiate an acquired resistance plant defense response constitutively in the absence of signals from the pathogen. The level of expression associated with such a plant defense response may be determined by measuring the levels of defense response gene expression as described herein or according to any conventional method. If  
5 desired, the AR transgenes are expressed by a controllable promoter such as a tissue-specific promoter, cell-type specific promoter, or by a promoter that is induced by an external signal or agent such as a pathogen- or wound-inducible control element, thus limiting the temporal or tissue expression or both of an acquired resistance defense response. The AR genes may also be expressed in roots, leaves, or fruits, or at a site of a plant that is susceptible to  
10 pathogen penetration and infection.

The invention is also useful for controlling plant disease by enhancing a plant's SAR defense mechanisms. In particular, the invention is useful for combating diseases known to be inhibited by plant SAR defense mechanisms. These include, without limitation, viral diseases caused by TMV and TNV, bacterial diseases caused by *Pseudomonas* and  
15 *Xanthomonas*, and fungal diseases caused by *Erysiphe*, *Peronospora*, *Phytophthora*, *Colletotrichum*, and *Magnaporthe grisea*. In particular exemplary approaches, constitutive or inducible expression of an AR gene in a transgenic plant is useful for controlling powdery mildew of wheat caused by *Erysiphe*, bacterial leaf spot of pepper caused by *Xanthomonas campestris*, bacterial wilt and bacterial spot of tomato caused by *Pseudomonas syringae* and  
20 *Xanthomonas campestris*, and bacterial blights of citrus and walnut caused by *Xanthomonas campestris*.

#### Other Embodiments

The invention further includes analogs of any naturally-occurring plant AR  
25 polypeptide. Analogs can differ from the naturally-occurring AR protein by amino acid sequence differences, by post-translational modifications, or by both. Analogs of the invention will generally exhibit at least 40%, more preferably 50%, and most preferably 60% or even having 70%, 80%, or 90% identity with all or part of a naturally-occurring plant AR amino acid sequence. The length of sequence comparison is at least 15 amino acid residues,  
30 preferably at least 25 amino acid residues, and more preferably more than 35 amino acid

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residues. Modifications include *in vivo* and *in vitro* chemical derivatization of polypeptides, e.g., acetylation, carboxylation, phosphorylation, or glycosylation; such modifications may occur during polypeptide synthesis or processing or following treatment with isolated modifying enzymes. Analogs can also differ from the naturally-occurring AR polypeptide by alterations in primary sequence. These include genetic variants, both natural and induced (for example, resulting from random mutagenesis by irradiation or exposure to ethyl methylsulfate or by site-specific mutagenesis as described in Sambrook, Fritsch and Maniatis, *Molecular Cloning: A Laboratory Manual* (2d ed.), CSH Press, 1989, or Ausubel et al., *supra*). Also included are cyclized peptides, molecules, and analogs which contain residues other than L-amino acids, e.g., D-amino acids or non-naturally occurring or synthetic amino acids, e.g.,  $\beta$  or  $\gamma$  amino acids.

In addition to full-length polypeptides, the invention also includes AR polypeptide fragments. As used herein, the term "fragment," means at least 20 contiguous amino acids, preferably at least 30 contiguous amino acids, more preferably at least 50 contiguous amino acids, and most preferably at least 60 to 80 or more contiguous amino acids. Fragments of AR polypeptides can be generated by methods known to those skilled in the art or may result from normal protein processing (e.g., removal of amino acids from the nascent polypeptide that are not required for biological activity or removal of amino acids by alternative mRNA splicing or alternative protein processing events). In preferred embodiments, an AR polypeptide fragment includes an ankyrin-repeat motif as described herein. In other preferred embodiments, an AR fragment is capable of interacting with a second polypeptide component of the AR signal transduction cascade.

Furthermore, the invention includes nucleotide sequences that facilitate specific detection of an AR nucleic acid. Thus, AR sequences described herein or portions thereof may be used as probes to hybridize to nucleotide sequences from other plants (e.g., dicots, monocots, gymnosperms, and algae) by standard hybridization techniques under conventional conditions. Sequences that hybridize to an AR coding sequence or its complement and that encode an AR polypeptide are considered useful in the invention. As used herein, the term "fragment," as applied to nucleic acid sequences, means at least 5 contiguous nucleotides, preferably at least 10 contiguous nucleotides, more preferably at least 20 to 30 contiguous



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nucleotides, and most preferably at least 40 to 80 or more contiguous nucleotides. Fragments of AR nucleic acid sequences can be generated by methods known to those skilled in the art.

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#### Deposit

Cosmids 21A4-2-1, 21A4-4-3-1, 21A4-P5-1 have been deposited with the American Type Culture Collection on July 8, 1996, and bear the accession numbers ATCC No. 97649, 97650, and 97651. Plasmid pKExNPR1 was deposited on July 31, 1996 and bears the  
10 accession number ATCC No. 97671. Applicants acknowledge their responsibility to replace these plasmids should it loose viability before the end of the term of a patent issued hereon, and their responsibility to notify the American Type Culture Collection of the issuance of such a patent, at which time the deposit will be made available to the public. Prior to that time the deposit will be made available to the Commissioner of Patents under terms of 37  
15 CFR § 1.14 and 35 USC § 112. These deposits are available as required by foreign patent laws in countries wherein counterparts of this subject application, or progeny, are filed. It should be understood that availability of a deposit does not constitute a license to practice the subject invention.

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All publications and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each independent publication or patent application was specifically and individually indicated to be incorporated by reference.

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## SEQUENCE LISTING

## (1) GENERAL INFORMATION

- (i) APPLICANT: The General Hospital Corporation et al.
- (ii) TITLE OF THE INVENTION:  
ACQUIRED RESISTANCE GENES AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 28
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Clark & Elbing LLP
  - (B) STREET: 176 Federal Street
  - (C) CITY: Boston
  - (D) STATE: MA
  - (E) COUNTRY: USA
  - (F) ZIP: 02110
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: PCT/US97/----
  - (B) FILING DATE: 08-AUG-97
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 60/023,851
  - (B) FILING DATE: August 9, 1996
  - (A) APPLICATION NUMBER: 60/035,166
  - (B) FILING DATE: January 10, 1997
  - (A) APPLICATION NUMBER: 60/046,769
  - (B) FILING DATE: May 16, 1997

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## (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Elbing, Karen L  
(B) REGISTRATION NUMBER: 35,238  
(C) REFERENCE/DOCKET NUMBER: 00786/339WO4

## (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 617-428-0200  
(B) TELEFAX: 617-428-7045

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7548 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Genomic DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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AAGCTTGTGA TGCAAGTCAT GGGATATTGC TTTGTGTTAA GTATACAAAA CCATCACGTG 60
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AGGGTTGGGA TATGTCATTG GGTTAGCGG TAATCGGATT GAACCCTTTC CGGTATAAAA 180
TACAAAGGCT TTCGCAGTCT CGGCGTATGT GTATGTCTCG GGGTATCTAC CATTTGAATC 240
ACAGAACTTT TATGTGCGAA GTTTTCGATT CTGATTCGTT TACCTGGAAG AGATTAGAAA 300
TTTGCGTCTA CAAAAACAG ACAGATTAAT TTTTCCAAC CCGATACAAG TTTCGGGGTT 360
CTTGCATTGG ATATCACGGA ACAACAATGT GATCCGGTTT TGTCTCAAAA CCGAAACTTG 420
GTCCTTCTTC CATACTCCGA ACTCTGATGT TTTCTCAGGA TTAGTCAGAT ACGAAGGGAA 480
GCTAGGTGCT ATTCGTCAGT GGACAAACAA AGATCAAGAA GATGTTACG AGTTATGGGT 540
TTAAAGAGC AGTTTTGAAA AGTCGTGGGT TAAAGTGAAA GATATTAAAA GCATTGGAGT 600
AGATTTGATT ACGTGGACTC CAAGCAACGA CGTTGTATTG TTTCGTAGTA GTGATCGTGG 660
TTGCCTCTAC AACATAAACG CAGAGAAGTT GAATTTAGTT TATGCAAAAA AAGAGGGATC 720
TGATTGTCTT TCGTTTGT TTCCGTTTTG TTCTGATTAC GAGAGGGTTG ATCTGAACGG 780
AAGAAGCAAC GGGCCGACAC TTTAAAAAAA AAATAAAAAA AATGGGCCGA CAAATGCAAA 840
CGTAGTTGAC AAGGATCTCA AGTCTCAAGT CTCAATTGGC TCGCTCATTG TGGGGCATAA 900
ATATATCTAG TGATGTTTAA TTGTTTTTAA TAAGGTAAAA AGGAATATTG AATTTTGTTT 960
CTTAGGTTTA TGTAATAATA CCAACATTG TTTTATGAAT ATTTAATCTG ATTTTTTGGC 1020
TAGTTATTTT ATTATATCAA GGGTTCCTGT TTATAGTTGA AAACAGTTAC TGTATAGAAA 1080
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 GTTATTGAAA AAGCTGATTT ATCGCATGAT TCAGAACGAG AAGTTGAAGG CAAATAACTA 1980  
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CCGGTGAAC AACTACAGGA TACTTACCAA AATATATTGA AACTGATTT CTGCAGCTGC 7140
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CCTTTCTCTC AAGGTTTCCA TCGCCATGAC CATAACAGTC CTGCAGTGAA TTCTAAGAAA 7320
AATGTAAAAA ATTTTGGCCT AAATCATAA TTCTTAACAT ACGAAACCAT GGAGAACTCC 7380
ATGTCTAAAA AATAAAGGCT AAAGCTTTTT GGCGACAGAA GCAGATAAAT CCATTCAAAA 7440
CACATAAACT CTAACAATA AACAGTGATA CTCAATACTA AGACTTGTAAG AGGTCTACGT 7500
AACTCAAAAC TGGAGAATTG TCAGATCGGG TGTGGCTAGT AGAAGCTT 7548

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## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 93...1871
- (D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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TCGATCTTTA ACCAAATCCA GTTGATAAGG TCTCTTCGTT GATTAGCAGA GATCTCTTTA	60
ATTTGTGAAT TTCAATTCAT CGGAACCTGT TG ATG GAC ACC ACC ATT GAT GGA	113
Met Asp Thr Thr Ile Asp Gly	
1 5	
TTC GCC GAT TCT TAT GAA ATC AGC AGC ACT AGT TTC GTC GCT ACC GAT	161
Phe Ala Asp Ser Tyr Glu Ile Ser Ser Thr Ser Phe Val Ala Thr Asp	
10 15 20	
AAC ACC GAC TCC TCT ATT GTT TAT CTG GCC GCC GAA CAA GTA CTC ACC	209
Asn Thr Asp Ser Ser Ile Val Tyr Leu Ala Ala Glu Gln Val Leu Thr	
25 30 35	
GGA CCT GAT GTA TCT GCT CTG CAA TTG CTC TCC AAC AGC TTC GAA TCC	257
Gly Pro Asp Val Ser Ala Leu Gln Leu Leu Ser Asn Ser Phe Glu Ser	
40 45 50 55	
GTC TTT GAC TCG CCG GAT GAT TTC TAC AGC GAC GCT AAG CTT GTT CTC	305
Val Phe Asp Ser Pro Asp Asp Phe Tyr Ser Asp Ala Lys Leu Val Leu	
60 65 70	
TCC GAC GGC CGG GAA GTT TCT TTC CAC CGG TGC GTT TTG TCA GCG AGA	353
Ser Asp Gly Arg Glu Val Ser Phe His Arg Cys Val Leu Ser Ala Arg	
75 80 85	
AGC TCT TTC TTC AAG AGC GCT TTA GCC GCC GCT AAG AAG GAG AAA GAC	401
Ser Ser Phe Phe Lys Ser Ala Leu Ala Ala Lys Lys Glu Lys Asp	
90 95 100	
TCC AAC AAC ACC GCC GCC GTG AAG CTC GAG CTT AAG GAG ATT GCC AAG	449
Ser Asn Asn Thr Ala Ala Val Lys Leu Glu Leu Lys Glu Ile Ala Lys	
105 110 115	
GAT TAC GAA GTC GGT TTC GAT TCG GTT GTG ACT GTT TTG GCT TAT GTT	497
Asp Tyr Glu Val Gly Phe Asp Ser Val Val Thr Val Leu Ala Tyr Val	
120 125 130 135	
TAC AGC AGC AGA GTG AGA CCG CCG CCT AAA GGA GTT TCT GAA TGC GCA	545
Tyr Ser Ser Arg Val Arg Pro Pro Pro Lys Gly Val Ser Glu Cys Ala	
140 145 150	
GAC GAG AAT TGC TGC CAC GTG GCT TGC CGG CCG GCG GTG GAT TTC ATG	593
Asp Glu Asn Cys Cys His Val Ala Cys Arg Pro Ala Val Asp Phe Met	
155 160 165	
TTG GAG GTT CTC TAT TTG GCT TTC ATC TTC AAG ATC CCT GAA TTA ATT	641
Leu Glu Val Leu Tyr Leu Ala Phe Ile Phe Lys Ile Pro Glu Leu Ile	
170 175 180	
ACT CTC TAT CAG AGG CAC TTA TTG GAC GTT GTA GAC AAA GTT GTT ATA	689
Thr Leu Tyr Gln Arg His Leu Leu Asp Val Val Asp Lys Val Val Ile	
185 190 195	
GAG GAC ACA TTG GTT ATA CTC AAG CTT GCT AAT ATA TGT GGT AAA GCT	737
Glu Asp Thr Leu Val Ile Leu Lys Leu Ala Asn Ile Cys Gly Lys Ala	
200 205 210 215	

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TGT ATG AAG CTA TTG GAT AGA TGT AAA GAG ATT ATT GTC AAG TCT AAT Cys Met Lys Leu Leu Asp Arg Cys Lys Glu Ile Ile Val Lys Ser Asn 220 225 230	785
GTA GAT ATG GTT AGT CTT GAA AAG TCA TTG CCG GAA GAG CTT GTT AAA Val Asp Met Val Ser Leu Glu Lys Ser Leu Pro Glu Glu Leu Val Lys 235 240 245	833
GAG ATA ATT GAT AGA CGT AAA GAG CTT GGT TTG GAG GTA CCT AAA GTA Glu Ile Ile Asp Arg Arg Lys Glu Leu Gly Leu Glu Val Pro Lys Val 250 255 260	881
AAG AAA CAT GTC TCG AAT GTA CAT AAG GCA CTT GAC TCG GAT GAT ATT Lys Lys His Val Ser Asn Val His Lys Ala Leu Asp Ser Asp Asp Ile 265 270 275	929
GAG TTA GTC AAG TTG CTT TTG AAA GAG GAT CAC ACC AAT CTA GAT GAT Glu Leu Val Lys Leu Leu Leu Lys Glu Asp His Thr Asn Leu Asp Asp 280 285 290 295	977
GCG TGT GCT CTT CAT TTC GCT GTT GCA TAT TGC AAT GTG AAG ACC GCA Ala Cys Ala Leu His Phe Ala Val Ala Tyr Cys Asn Val Lys Thr Ala 300 305 310	1025
ACA GAT CTT TTA AAA CTT GAT CTT GCC GAT GTC AAC CAT AGG AAT CCG Thr Asp Leu Leu Lys Leu Asp Leu Ala Asp Val Asn His Arg Asn Pro 315 320 325	1073
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TTG GAA GGT AGA ACC GCA CTC ATG ATC GCA AAA CAA GCC ACT ATG GCG Leu Glu Gly Arg Thr Ala Leu Met Ile Ala Lys Gln Ala Thr Met Ala 360 365 370 375	1217
GTT GAA TGT AAT AAT ATC CCG GAG CAA TGC AAG CAT TCT CTC AAA GGC Val Glu Cys Asn Asn Ile Pro Glu Gln Cys Lys His Ser Leu Lys Gly 380 385 390	1265
CGA CTA TGT GTA GAA ATA CTA GAG CAA GAA GAC AAA CGA GAA CAA ATT Arg Leu Cys Val Glu Ile Leu Glu Gln Glu Asp Lys Arg Glu Gln Ile 395 400 405	1313
CCT AGA GAT GTT CCT CCC TCT TTT GCA GTG GCG GCC GAT GAA TTG AAG Pro Arg Asp Val Pro Pro Ser Phe Ala Val Ala Ala Asp Glu Leu Lys 410 415 420	1361
ATG ACG CTG CTC GAT CTT GAA AAT AGA GTT GCA CTT GCT CAA CGT CTT Met Thr Leu Leu Asp Leu Glu Asn Arg Val Ala Leu Ala Gln Arg Leu 425 430 435	1409
TTT CCA ACG GAA GCA CAA GCT GCA ATG GAG ATC GCC GAA ATG AAG GGA Phe Pro Thr Glu Ala Gln Ala Ala Met Glu Ile Ala Glu Met Lys Gly 440 445 450 455	1457

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ACA TGT GAG TTC ATA GTG ACT AGC CTC GAG CCT GAC CGT CTC ACT GGT Thr Cys Glu Phe Ile Val Thr Ser Leu Glu Pro Asp Arg Leu Thr Gly 460 465 470	1505
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GAA GAG CAT CAA AGT AGA CTA AAA GCG CTT TCT AAA ACC GTG GAA CTC Glu Lys His Gln Ser Arg Leu Lys Ala Leu Ser Lys Thr Val Glu Leu 490 495 500	1601
GGG AAA CGA TTC TTC CCG CGC TGT TCG GCA GTG CTC GAC CAG ATT ATG Gly Lys Arg Phe Phe Pro Arg Cys Ser Ala Val Leu Asp Gln Ile Met 505 510 515	1649
AAC TGT GAG GAC TTG ACT CAA CTG GCT TGC GGA GAA GAC GAC ACT GCT Asn Cys Glu Asp Leu Thr Gln Leu Ala Cys Gly Glu Asp Asp Thr Ala 520 525 530 535	1697
GAG AAA CGA CTA CAA AAG AAG CAA AGG TAC ATG GAA ATA CAA GAG ACA Glu Lys Arg Leu Gln Lys Lys Gln Arg Tyr Met Glu Ile Gln Glu Thr 540 545 550	1745
CTA AAG AAG GCC TTT AGT GAG GAC AAT TTG GAA TTA GGA AAT TCG TCC Leu Lys Lys Ala Phe Ser Glu Asp Asn Leu Glu Leu Gly Asn Ser Ser 555 560 565	1793
CTG ACA GAT TCG ACT TCT TCC ACA TCG AAA TCA ACC GGT GGA AAG AGG Leu Thr Asp Ser Thr Ser Ser Thr Ser Lys Ser Thr Gly Gly Lys Arg 570 575 580	1841
TCT AAC CGT AAA CTC TCT CAT CGT CGT CGG TGAGACTCTT GCCTCTTAGT GTA Ser Asn Arg Lys Leu Ser His Arg Arg Arg 585 590	1894
ATTTTGTGCTG TACCATATAA TTCTGTTTTT ATGATGACTG TAACTGTTTA TGTCTATCGT TGGCGTCATA TAGTTTCGCT CTTCGTTTTG CATCCTGTGT ATTATTGCTG CAGGTGTGCT TCAAACAAAT GTTGTAACAA TTTGAACCAA TGGTATACAG ATTTGTAATA TATATTTATG TACATCAACA ATAAAAAAAA AAAAAAAAAA	1954 2014 2074 2104

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 593 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Asp Thr Thr Ile Asp Gly Phe Ala Asp Ser Tyr Glu Ile Ser Ser  
1 5 10 15



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Thr Ser Phe Val Ala Thr Asp Asn Thr Asp Ser Ser Ile Val Tyr Leu  
 20 25 30  
 Ala Ala Glu Gln Val Leu Thr Gly Pro Asp Val Ser Ala Leu Gln Leu  
 35 40 45  
 Leu Ser Asn Ser Phe Glu Ser Val Phe Asp Ser Pro Asp Asp Phe Tyr  
 50 55 60  
 Ser Asp Ala Lys Leu Val Leu Ser Asp Gly Arg Glu Val Ser Phe His  
 65 70 75 80  
 Arg Cys Val Leu Ser Ala Arg Ser Ser Phe Phe Lys Ser Ala Leu Ala  
 85 90 95  
 Ala Ala Lys Lys Glu Lys Asp Ser Asn Asn Thr Ala Ala Val Lys Leu  
 100 105 110  
 Glu Leu Lys Glu Ile Ala Lys Asp Tyr Glu Val Gly Phe Asp Ser Val  
 115 120 125  
 Val Thr Val Leu Ala Tyr Val Tyr Ser Ser Arg Val Arg Pro Pro Pro  
 130 135 140  
 Lys Gly Val Ser Glu Cys Ala Asp Glu Asn Cys Cys His Val Ala Cys  
 145 150 155 160  
 Arg Pro Ala Val Asp Phe Met Leu Glu Val Leu Tyr Leu Ala Phe Ile  
 165 170 175  
 Phe Lys Ile Pro Glu Leu Ile Thr Leu Tyr Gln Arg His Leu Leu Asp  
 180 185 190  
 Val Val Asp Lys Val Val Ile Glu Asp Thr Leu Val Ile Leu Lys Leu  
 195 200 205  
 Ala Asn Ile Cys Gly Lys Ala Cys Met Lys Leu Leu Asp Arg Cys Lys  
 210 215 220  
 Glu Ile Ile Val Lys Ser Asn Val Asp Met Val Ser Leu Glu Lys Ser  
 225 230 235 240  
 Leu Pro Glu Glu Leu Val Lys Glu Ile Ile Asp Arg Arg Lys Glu Leu  
 245 250 255  
 Gly Leu Glu Val Pro Lys Val Lys Lys His Val Ser Asn Val His Lys  
 260 265 270  
 Ala Leu Asp Ser Asp Asp Ile Glu Leu Val Lys Leu Leu Lys Glu  
 275 280 285  
 Asp His Thr Asn Leu Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala  
 290 295 300  
 Tyr Cys Asn Val Lys Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala  
 305 310 315 320  
 Asp Val Asn His Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala  
 325 330 335  
 Ala Met Arg Lys Glu Pro Gln Leu Ile Leu Ser Leu Leu Glu Lys Gly  
 340 345 350  
 Ala Ser Ala Ser Glu Ala Thr Leu Glu Gly Arg Thr Ala Leu Met Ile  
 355 360 365  
 Ala Lys Gln Ala Thr Met Ala Val Glu Cys Asn Asn Ile Pro Glu Gln  
 370 375 380  
 Cys Lys His Ser Leu Lys Gly Arg Leu Cys Val Glu Ile Leu Glu Gln  
 385 390 395 400  
 Glu Asp Lys Arg Glu Gln Ile Pro Arg Asp Val Pro Pro Ser Phe Ala  
 405 410 415  
 Val Ala Ala Asp Glu Leu Lys Met Thr Leu Leu Asp Leu Glu Asn Arg  
 420 425 430  
 Val Ala Leu Ala Gln Arg Leu Phe Pro Thr Glu Ala Gln Ala Ala Met  
 435 440 445  
 Glu Ile Ala Glu Met Lys Gly Thr Cys Glu Phe Ile Val Thr Ser Leu  
 450 455 460  
 Glu Pro Asp Arg Leu Thr Gly Thr Lys Arg Thr Ser Pro Gly Val Lys  
 465 470 475 480  
 Ile Ala Pro Phe Arg Ile Leu Glu Glu His Gln Ser Arg Leu Lys Ala  
 485 490 495

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Leu Ser Lys Thr Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser  
           500          505          510  
 Ala Val Leu Asp Gln Ile Met Asn Cys Glu Asp Leu Thr Gln Leu Ala  
           515          520          525  
 Cys Gly Glu Asp Asp Thr Ala Glu Lys Arg Leu Gln Lys Lys Gln Arg  
           530          535          540  
 Tyr Met Glu Ile Gln Glu Thr Leu Lys Lys Ala Phe Ser Glu Asp Asn  
           545          550          555          560  
 Leu Glu Leu Gly Asn Ser Ser Leu Thr Asp Ser Thr Ser Ser Thr Ser  
           565          570          575  
 Lys Ser Thr Gly Gly Lys Arg Ser Asn Arg Lys Leu Ser His Arg Arg  
           580          585          590  
 Arg

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asn His Arg Asn Pro Arg Gly Tyr Thr Val Leu His Val Ala Ala Met  
   1          5          10          15  
 Arg Lys Glu Pro Gln Leu Ile Leu Ser Leu Leu Glu Lys Gly Ala Ser  
           20          25          30  
 Ala Ser Glu Ala Thr Leu Glu Gly Arg Thr Ala Leu Met Ile Ala Lys  
           35          40          45  
 Gln

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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Asn Ala Lys Thr Lys Asn Gly Tyr Thr Ala Leu His Gln Ala Ala Gln  
1 5 10 15  
Gln Gly His Thr His Ile Ile Asn Val Leu Leu Gln Asn Asn Ala Ser  
20 25 30  
Pro Asn Glu Leu Thr Val Asn Gly Asn Thr Ala Leu Ala Ile Ala Arg  
35 40 45  
Arg

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Val Lys Lys His Val Ser Asn Val His Lys Ala Leu Asp Ser Asp  
1 5 10 15  
Asp Ile Glu Leu Val Lys Leu Leu Leu Lys Glu Asp  
20 25

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Lys Thr Lys Asn Gly Leu Ser Pro Leu His Met Ala Thr Gln Gly Asp  
1 5 10 15  
His Leu Asn Cys Val Gln Leu Leu Leu Ser Arg Asn  
20 25

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids

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- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Lys His Val Ser Asn Val His Lys Ala Leu Asp Ser Asp Asp Ile Glu  
 1            5            10            15  
 Leu Val Lys Leu Leu Leu Lys Glu Asp His Thr Asn Leu Asp Asp Ala  
           20            25       /       30  
 Cys

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Asp Ala Cys Ala Leu His Phe Ala Val Ala Tyr Cys Asn Val Lys  
 1            5            10            15  
 Thr Ala Thr Asp Leu Leu Lys Leu Asp Leu Ala Asp Val Asn His Arg  
           20            25            30  
 Asn

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 33 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Arg Gly Tyr Thr Val Leu His Val Ala Ala Met Arg Lys Glu Pro Gln  
 1            5            10            15

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Leu Ile Leu Ser Leu Leu Glu Lys Gly Ala Ser Ala Ser Glu Ala Thr  
           20              25              30  
 Leu

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Glu Gly Arg Thr Ala Leu Met Ile Ala Lys Gln Ala Thr Met Ala Val  
   1          5          10          15  
 Glu Cys Asn Asn Ile Pro Glu Gln Cys Lys His Ser Leu Lys Gly Arg  
           20          25          30  
 Leu

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly Thr Pro Leu His Leu Ala Ala Arg Gly His Val Glu Val Val Lys  
   1          5          10          15  
 Leu Leu Leu Asp Gly Ala Asp Val Asn Ala Thr Lys Ala Ile Ser Gln  
           20          25          30  
 Asn Asn Leu Asp Ile Ala Glu Val Lys Asn Pro Asp Asp Val Lys Thr  
           35          40          45  
 Met Arg Gln Ser Ile Asn Glu  
           50          55

## (2) INFORMATION FOR SEQ ID NO:13:

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
GTGACTTTCT AACTATGGCT GAAATTGCAG AACGAAAAAG ACTTTCCATT TTTCACTTGA      60
ATGAAACCCA AAATGGAAAT CTATCTCTCT TCTTCTCTC TTTTACTACC TCCATTTCCA      120
TGGCTTTCCC TCCTCTACCT TCCCTAGCTC TTTTCAATTT CTAGAATATT CTTTCTTAG      180
TCTGTAATTA TCTATAGCTC AATTTCTAAG ACAGAACTTA TGTAAGGCGG CTTTCTGTAA      240
TGGATAATAG TAGGACTGCG TTTTCTGATT CGAATGACAT CAGCGGAAGC AGTAGTATAT      300
GCTGCATCGG CGCGGGCATG ACTGAATTTT TCTCGCCGGA GACTTCGCCG GCGGAGATCA      360
CTTCACTGAA ACGCCTATCG GAAACACTGG AATCTATCTT CGATGCGTCT TTGCCGGAGT      420
TTGACTACTT CGCCGACGCT AAGCTTGTGG TTCCGGCCC GTGTAAGGAA ATTCCGGTGC      480
ACCGGTGCAT TTTGTCGGCG AGGAGTCCGT TCTTAAAGAA TTTGTTCTGC GGTA AAAAAGG      540
AGAAGAATAG TAGTAAGGTG GAATTGAAGG AGGTGATGAA AGAGCATGAG GTGAGCTATG      600
ATGCTGTAAT GAGTGTATTG GCTTATTTGT ATAGTGGTAA AGTTAGGCCT TCACCTAAAG      660
ATGTGTGTGT TTGTGTGGAC AATGACTGCT CTCATGTGGC TTGTAGGCCA GCTGTGGCAT      720
TCCTGGTTGA GGTTTTGTAC ACATCATTTA CCTTTCAGAT CTCTGAATTG GTTGACAAGT      780
TTCAGAGACA CCTACTGGAT ATTCTTGACA AAAGTGCAGC AGACGATGTA ATGATGGTTT      840
TATCTGTTGC AAACATTTGT GGTAAGCAT GCGAGAGATT GCTTCAAGC TGCATTGAGA      900
TTATTGTCAA GTCTAATGTT GATATCATAA CCCTTGATAA AGCCTTGCCT CATGACATTG      960
TAAAACAAAT TACTGATTCA CGAGCGGAAC TTGGTCTACA AGGGCCTGAA AGCAACGGTT      1020
TTCCTGATAA ACATGTTAAG AGGATACATA GGGCATTGGA TTCTGATGAT GTTGAATTAC      1080
TACAAATGTT GCTAAGAGAG GGGCATACTA CCCTAGATGA TGCATATGCT CTCCATTATG      1140
CTGTAGCGTA TTGCGATGCA AAGACTACAG CAGAACTTCT AGATCTTGCA CTTGCTGATA      1200
TTAATCATCA AAATTCAAGG GGATACACGG TGCTGCATGT TGCAGCCATG AGGAAAGAGC      1260
CTAAAATTGT AGTGTCCTT TTAACCAAAG GAGCTAGACC TTCTGATCTG ACATCCGATG      1320
GAAGAAAAGC ACTTCAAATC GCCAAGAGGC TCACTAGGCT TGTGGATTTC AGTAAGTCTC      1380
CGGAGGAAGG AAAATCTGCT TCGAATGATC GGTTATGCAT TGAGATTCTG GAGCAAGCAG      1440
AAAGAAGAGA CCCTCTGCTA GGAGAAGCTT CTGTATCTCT TGCTATGGCA GCGGATGATT      1500
TGCGTATGAA GCTGTTATAC CTTGAAAATA GAGTTGGCCT GGCTAAACTC CTTTTTCCAA      1560
TGGAAGCTAA AGTTGCAATG GACATTGCTC AAGTTGATGG CACTTCTGAG TTCCCACTGG      1620
CTAGCATCGG CAAAAGATG GCTAATGCAC AGAGGACAAC AGTAGATTG AACGAGGCTC      1680
CTTTCAAGAT AAAAGAGGAG CACTTGAATC GGCTTAGAGC ACTCTCTAGA CTGTAGAAC      1740
TTGGAACACG CTTCTTTCCA CGTTGTTTCA AAGTTCTAAA TAAGATCATG GATGCTGATG      1800
ACTTGTCTGA GATAGCTTAC ATGGGGAATG ATACGGCAGA AGAGCGTCAA CTGAAGAAGC      1860
AAAGGTACAT GGAACCTCAA GAAATCTGTA CTAAAGCATT CACTGAGGAT AAAGAAGAAT      1920
ATGATAAGAC TAACAACATC TCCTCATCTT GTTCCTCTAC ATCTAAGGGA GTAGATAAGC      1980
CCAATAAGCT CCCTTTTAGG AAATAGGTAA TTGTATTAGG ATATATGAGG AAGAAGAGGA      2040
TTTTCTGTA ACATAGCACT CTTTCCTTTC ATCATTTGAT ATGTCAACAT ACATACAACA      2100
GCTGTACCAT AAACCTGTAT TGTGCACTT ACAACTTTGA AGAACAGAAT TTATTTGAAA      2160
AAAAAAAAAA AA
```

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Asp Asn Ser Arg Thr Ala Phe Ser Asp Ser Asn Asp Ile Ser Gly  
1 5 10 15  
Ser Ser Ser Ile Cys Cys Ile Gly Gly Gly Met Thr Glu Phe Phe Ser  
20 25 30  
Pro Glu Thr Ser Pro Ala Glu Ile Thr Ser Leu Lys Arg Leu Ser Glu  
35 40 45  
Thr Leu Glu Ser Ile Phe Asp Ala Ser Leu Pro Glu Phe Asp Tyr Phe  
50 55 60  
Ala Asp Ala Lys Leu Val Val Ser Gly Pro Cys Lys Glu Ile Pro Val  
65 70 75 80  
His Arg Cys Ile Leu Ser Ala Arg Ser Pro Phe Phe Lys Asn Leu Phe  
85 90 95  
Cys Gly Lys Lys Glu Lys Asn Ser Ser Lys Val Glu Leu Lys Glu Val  
100 105 110  
Met Lys Glu His Glu Val Ser Tyr Asp Ala Val Met Ser Val Leu Ala  
115 120 125  
Tyr Leu Tyr Ser Gly Lys Val Arg Pro Ser Pro Lys Asp Val Cys Val  
130 135 140  
Cys Val Asp Asn Asp Cys Ser His Val Ala Cys Arg Pro Ala Val Ala  
145 150 155 160  
Phe Leu Val Glu Val Leu Tyr Thr Ser Phe Thr Phe Gln Ile Ser Glu  
165 170 175  
Leu Val Asp Lys Phe Gln Arg His Leu Leu Asp Ile Leu Asp Lys Thr  
180 185 190  
Ala Ala Asp Asp Val Met Met Val Leu Ser Val Ala Asn Ile Cys Gly  
195 200 205  
Lys Ala Cys Glu Arg Leu Leu Ser Ser Cys Ile Glu Ile Ile Val Lys  
210 215 220  
Ser Asn Val Asp Ile Ile Thr Leu Asp Lys Ala Leu Pro His Asp Ile  
225 230 235 240  
Val Lys Gln Ile Thr Asp Ser Arg Ala Glu Leu Gly Leu Gln Gly Pro  
245 250 255  
Glu Ser Asn Gly Phe Pro Asp Lys His Val Lys Arg Ile His Arg Ala  
260 265 270  
Leu Asp Ser Asp Asp Val Glu Leu Leu Gln Met Leu Leu Arg Glu Gly  
275 280 285  
His Thr Thr Leu Asp Asp Ala Tyr Ala Leu His Tyr Ala Val Ala Tyr  
290 295 300

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Cys Asp Ala Lys Thr Thr Ala Glu Leu Leu Asp Leu Ala Leu Ala Asp  
 305                      310                      315                      320  
 Ile Asn His Gln Asn Ser Arg Gly Tyr Thr Val Leu His Val Ala Ala  
                     325                      330                      335  
 Met Arg Lys Glu Pro Lys Ile Val Val Ser Leu Leu Thr Lys Gly Ala  
                     340                      345                      350  
 Arg Pro Scr Asp Leu Thr Ser Asp Gly Arg Lys Ala Leu Gln Ile Ala  
                     355                      360                      365  
 Lys Arg Leu Thr Arg Leu Val Asp Phe Ser Lys Ser Pro Glu Glu Gly  
                     370                      375                      380  
 Lys Ser Ala Ser Asn Asp Arg Leu Cys Ile Glu Ile Leu Glu Gln Ala  
 385                      390                      395                      400  
 Glu Arg Arg Asp Pro Leu Leu Gly Glu Ala Ser Val Ser Leu Ala Met  
                     405                      410                      415  
 Ala Gly Asp Asp Leu Arg Met Lys Leu Leu Tyr Leu Glu Asn Arg Val  
                     420                      425                      430  
 Gly Leu Ala Lys Leu Leu Phe Pro Met Glu Ala Lys Val Ala Met Asp  
                     435                      440                      445  
 Ile Ala Gln Val Asp Gly Thr Ser Glu Phe Pro Leu Ala Ser Ile Gly  
                     450                      455                      460  
 Lys Lys Met Ala Asn Ala Gln Arg Thr Thr Val Asp Leu Asn Glu Ala  
 465                      470                      475                      480  
 Pro Phe Lys Ile Lys Glu Glu His Leu Asn Arg Leu Arg Ala Leu Ser  
                     485                      490                      495  
 Arg Thr Val Glu Leu Gly Lys Arg Phe Phe Pro Arg Cys Ser Glu Val  
                     500                      505                      510  
 Leu Asn Lys Ile Met Asp Ala Asp Asp Leu Ser Glu Ile Ala Tyr Met  
                     515                      520                      525  
 Gly Asn Asp Thr Ala Glu Glu Arg Gln Leu Lys Lys Gln Arg Tyr Met  
                     530                      535                      540  
 Glu Leu Gln Glu Ile Leu Thr Lys Ala Phe Thr Glu Asp Lys Glu Glu  
 545                      550                      555                      560  
 Tyr Asp Lys Thr Asn Asn Ile Ser Ser Ser Cys Ser Ser Thr Ser Lys  
                     565                      570                      575  
 Gly Val Asp Lys Pro Asn Lys Leu Pro Phe Arg Lys  
                     580                      585

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



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(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTGACAGACT TGCTCCTACT G

21

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CAGTGTGTAT CAAAGCACCA

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTCTCCAGAC CACATGATTA T

21

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

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TGAAGCTAAT ATGCACAGGA G

21

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTAGGTGCTC TTGTTCTTCC C

21

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CACATAATTC CCACGAGGAT C

21

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Lys Gly Thr Cys Glu Phe Ile Val Thr Ser Leu Glu Pro Asp Arg

1            5            10            15

Leu

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## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Arg Arg Lys Glu Leu Gly Leu Glu Val Pro Lys Val Lys Lys  
1           5           10

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Lys Lys Gln Arg Tyr Met Glu Ile Gln Glu Thr Leu Lys Lys  
1           5           10

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AARGARGAYC AYACNAA

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## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TAYGTYAAYG TNAARAC

17

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCCATNGTNG CYTGYTT

17

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AARGTNAARA ARCA YGT

17

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

RAAYTCRCAN GTNCCYTTCA T

21

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We claim:

Claims

1. An isolated nucleic acid molecule comprising a sequence encoding an acquired resistance polypeptide, wherein said acquired resistance polypeptide is capable of conferring, on a plant expressing said polypeptide, resistance to a plant pathogen.
2. The isolated nucleic acid molecule of claim 1, wherein said polypeptide is capable of mediating the expression of a pathogenesis-related polypeptide.
3. The isolated nucleic acid molecule of claim 1, wherein said polypeptide comprises an ankyrin-repeat motif.
4. The isolated nucleic acid molecule of claim 1, wherein said polypeptide is obtained from an angiosperm.
5. The isolated nucleic acid molecule of claim 4, wherein said angiosperm is a member of the *Solanaceae* or the *Cruciferae*.
6. The isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule is genomic DNA or cDNA.
7. The isolated nucleic acid molecule of claim 1, wherein said plant pathogen is a bacterium, virus, viroid, fungus, nematode, or insect.
8. An isolated nucleic acid molecule that encodes an acquired resistance polypeptide that specifically hybridizes to a nucleic acid molecule comprising the genomic nucleic acid sequence of Fig. 4 (SEQ ID NO:1).
9. An isolated nucleic acid molecule that encodes an acquired resistance polypeptide that specifically hybridizes to a nucleic acid molecule comprising the cDNA of Fig. 5 (SEQ ID NO:2).

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10. An isolated nucleic acid molecule that encodes an acquired resistance polypeptide that specifically hybridizes to a nucleic acid molecule comprising CDNA sequence of Fig. 7A (SEQ ID NO:13).

5           11. The isolated nucleic acid molecule of claims 8-10, wherein said nucleic acid molecule encodes a polypeptide that mediates the expression of a pathogenesis-related polypeptide.

10           12. The isolated nucleic acid molecule of claims 8-10, wherein said nucleic acid molecule encodes a polypeptide comprising an ankyrin-repeat motif.

13. The isolated nucleic acid molecule of claims 1 or 8-10, wherein said nucleic acid molecule is operably linked to an expression control region.

15           14. A vector comprising the nucleic acid molecule of claims 1 or 8-10, said vector being capable of directing expression of the polypeptide encoded by said nucleic acid molecule.

20           15. A cell comprising an isolated nucleic acid molecule of claims 1, 8-10, or 14.

16. The cell of claim 15, wherein said cell is a plant cell.

17. The cell of claim 15, wherein said cell is a bacterial cell.

25           18. The cell of claim 17, wherein said bacterial cell is *Agrobacterium*.

19. The cell of claim 16, wherein said plant cell has increased resistance to a plant pathogen.

30           20. A transgenic plant comprising a nucleic acid molecule of claim 1, 8-10, or 14,



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wherein said nucleic acid molecule is expressed in said transgenic plant.

21. The transgenic plant of claim 20, wherein said transgenic plant is an angiosperm.

22. The transgenic plant of claim 20, wherein said transgenic angiosperm is a monocot or a dicot.

23. The transgenic plant of claim 20, wherein said dicot is a cruciferous plant or a solanaceous plant.

24. A seed from a transgenic plant of claim 20.

25. A cell from a transgenic plant of claim 20.

26. A substantially pure acquired resistance polypeptide including an amino acid sequence that has at least 40% identity to the amino acid sequence of Fig. 5 (SEQ ID NO:3) or Fig. 7B (SEQ ID NO:14).

27. The substantially pure polypeptide of claim 26, wherein said polypeptide is capable of mediating the expression of a pathogenesis-related polypeptide.

28. The substantially pure polypeptide of claim 26, wherein said polypeptide includes an ankyrin-repeat motif or a G-protein coupled receptor motif.

29. The substantially pure polypeptide of claim 26, wherein said polypeptide is obtained from an angiosperm.

30. The substantially pure polypeptide of claim 29, wherein said angiosperm is a member of the *Solanaceae* or the *Cruciferae*.

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31. A method of producing an acquired resistance polypeptide, said method comprising the steps of:

(a) providing a cell transformed with a nucleic acid molecule of claims 1 or 8-10 positioned for expression in the cell;

5 (b) culturing the transformed cell under conditions for expressing the nucleic acid molecule; and

(c) recovering the acquired resistance polypeptide.

10 32. A recombinant acquired resistance polypeptide produced by the method of claim 31.

33. A substantially pure antibody that specifically recognizes and binds to an acquired resistance polypeptide or a portion thereof.

15 34. The substantially pure antibody of claim 33, wherein said antibody recognizes and binds to a recombinant acquired resistance polypeptide or a portion thereof.

35. A method of providing an increased level of resistance against a disease caused by a plant pathogen in a transgenic plant, said method comprising the steps of:

20 (a) producing a transgenic plant cell including the nucleic acid molecule of claims 1 or 8-10, wherein said nucleic acid is positioned for expression in the plant cell; and

(b) growing a transgenic plant from the plant cell wherein the nucleic acid molecule is expressed in the transgenic plant and the transgenic plant is thereby provided with an increased level of resistance against a disease caused by a plant pathogen.

25

36. The method of claim 35, wherein said plant pathogen is a bacterium, virus, viroid, fungus, nematode, or insect.

30 37. The method of claim 35, wherein said plant pathogen is *Phytophthora*, *Peronospora*, or *Pseudomonas*.

38. A method of isolating an acquired resistance gene or fragment thereof, said method comprising the steps of:

- (a) contacting the nucleic acid molecule of Fig. 4 (SEQ ID NO:1), Fig. 5 (SEQ ID NO:2), or Fig. 7A (SEQ ID NO:13) or a portion thereof with a preparation of DNA from a plant cell under hybridization conditions providing detection of DNA sequences having at least 40% or greater sequence identity to the nucleic acid sequence of Fig. 4 (SEQ ID NO:1), Fig. 5 (SEQ ID NO:2), or Fig. 7A (SEQ ID NO:13); and
- (b) isolating said hybridizing DNA.

39. A method of isolating an acquired resistance gene or fragment thereof, said method comprising the steps of:

- (a) providing a sample of plant cell DNA;
- (b) providing a pair of oligonucleotides having sequence identity to a region of the nucleic acid of Fig. 4 (SEQ ID NO:1), Fig. 5 (SEQ ID NO:2), or Fig. 7A (SEQ ID NO:13);
- (c) contacting the pair of oligonucleotides with said plant cell DNA under conditions suitable for polymerase chain reaction-mediated DNA amplification; and
- (d) isolating the amplified acquired resistance gene or fragment thereof.

40. The method of claim 39, wherein said amplification step is carried out using a sample of cDNA prepared from a plant cell.

41. The method of claim 39, wherein said pair of oligonucleotides are based on a sequence encoding an acquired resistance polypeptide, wherein the acquired resistance polypeptide is at least 40% identical to the amino acid sequence of Fig. 5 (SEQ ID NO:3) or Fig. 7B (SEQ ID NO:14).

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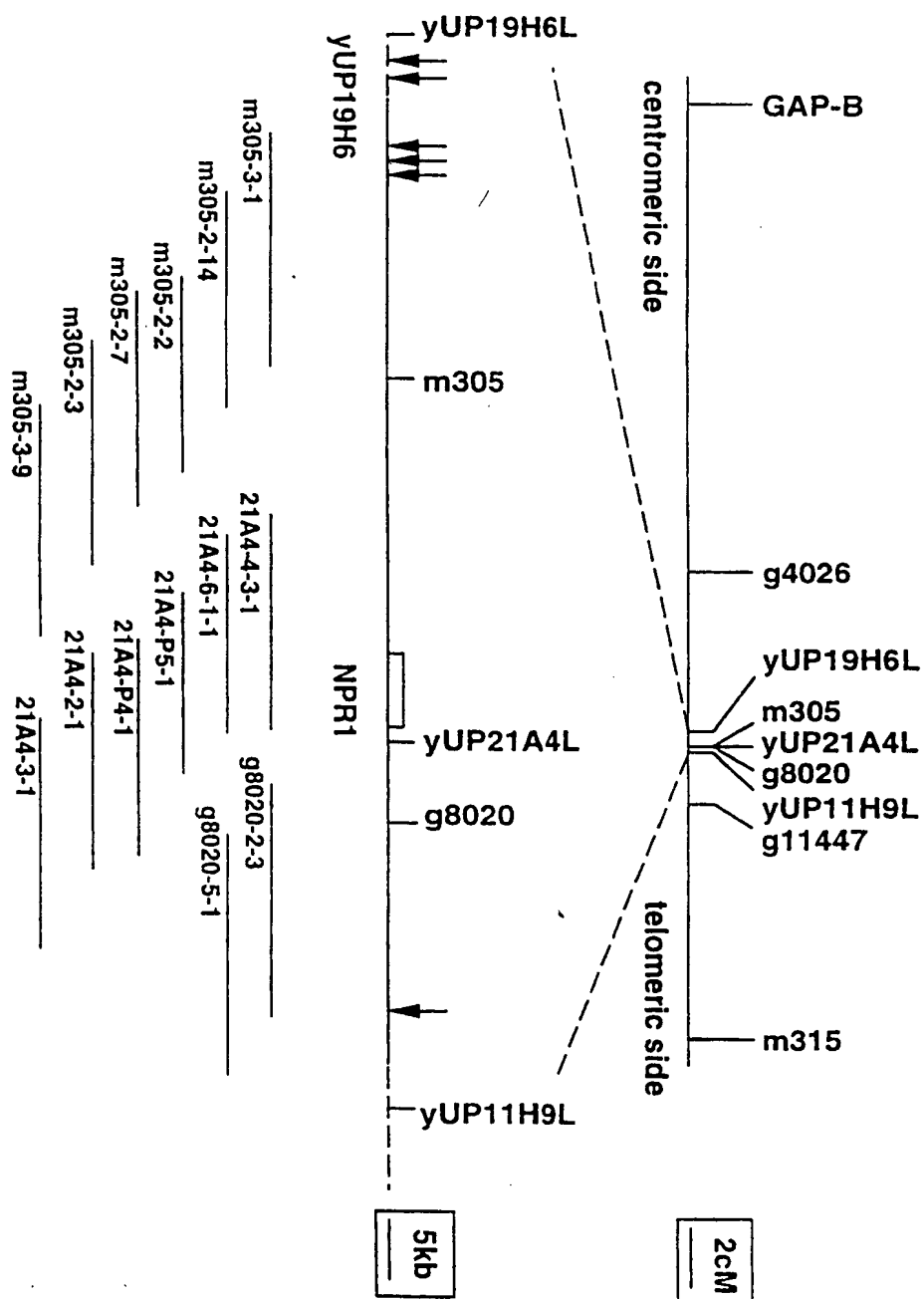


FIG. 2A

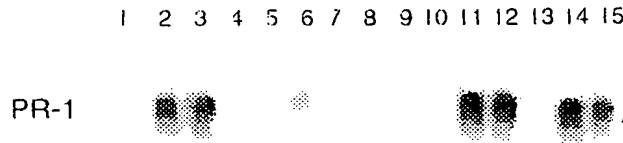


FIG. 2B

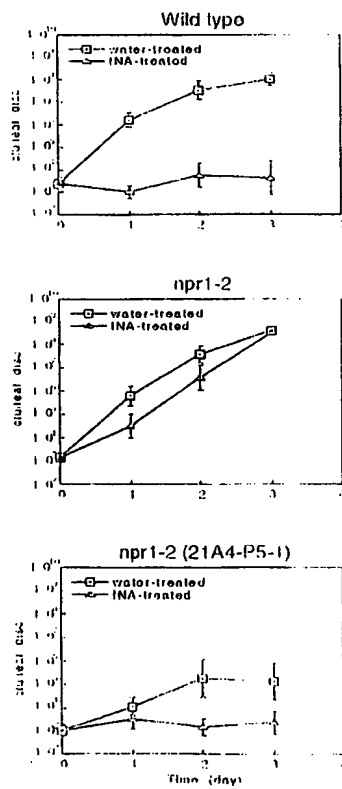


FIG. 2C

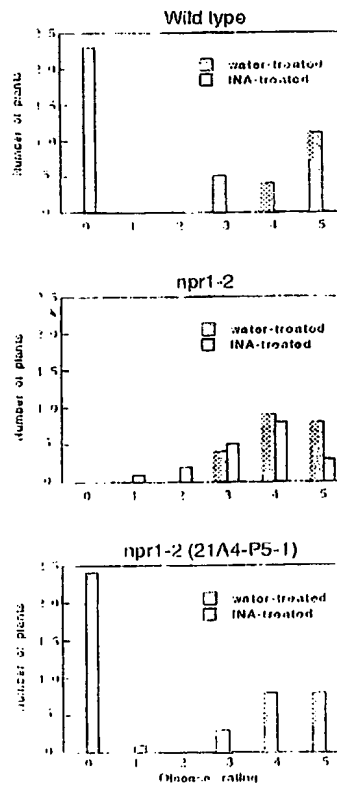


FIG. 2D

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# Restriction Map of the *NPR1* Locus (7547 bp)

## Unique Sites

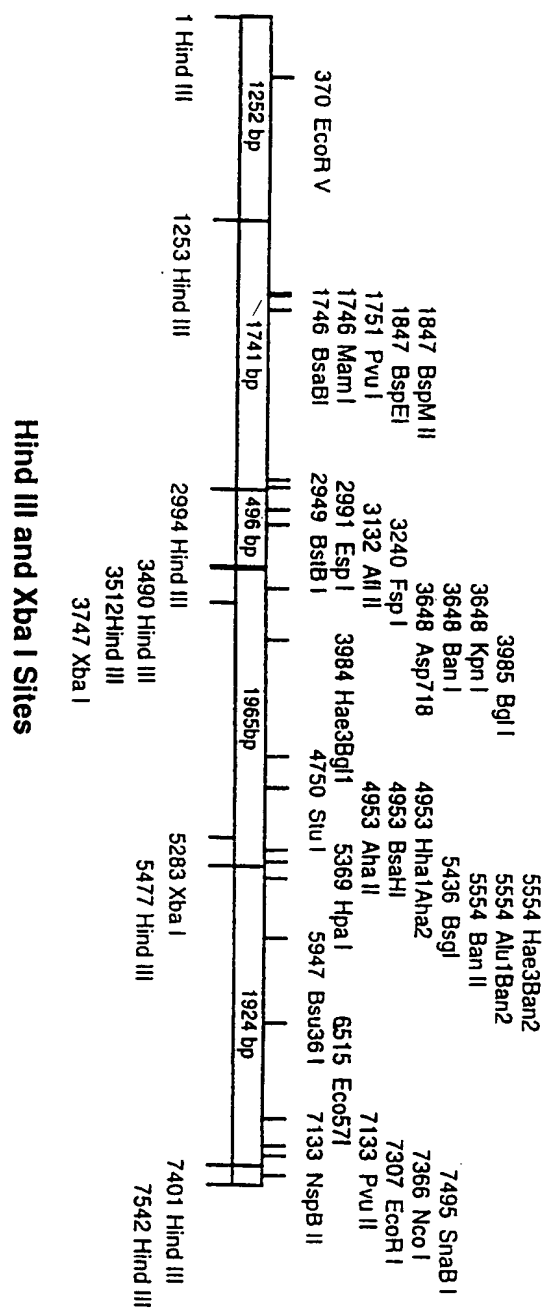


FIG. 3

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10	20	30	40	50
*	*	*	*	*
AAGCTTGTGA	TGCAAGTCAT	GGGATATTGC	TTTGTGTAA	GTATACAAAA
TTCGAACACT	ACGTTTCAGTA	CCCTATAACG	AAACACAATT	CATATGTTTT
60	70	80	90	100
*	*	*	*	*
CCATCACGTG	GATACATAGT	CTTCAAACCA	ACCACTAAAC	AGTATCAGGT
GGTAGTGAC	CTATGTATCA	GAAGTTTGGT	TGGTGATTG	TCATAGTCCA
110	120	130	140	150
*	*	*	*	*
CATACCAAAG	CCAGAAGTGA	AGGGTTGGGA	TATGTCATTG	GGTTTAGCGG
GTATGGTTTC	GGTCTTCACT	TCCCAACCCT	ATACAGTAAC	CCAAATCGCC
160	170	180	190	200
*	*	*	*	*
TAATCGGATT	GAACCCTTTC	CGGTATAAAA	TACAAAGGCT	TTCGCAGTCT
ATTAGCCTAA	CTTGGGAAAG	GCCATATTTT	ATGTTTCCGA	AAGCGTCAGA
210	220	230	240	250
*	*	*	*	*
CGGCGTATGT	GTATGTCTCG	GGGTATCTAC	CATTTGAATC	ACAGAACTTT
GCCGCATACA	CATACAGAGC	CCCATAGATG	GTAAACTTAG	TGTCTTGAAA
260	270	280	290	300
*	*	*	*	*
TATGTGCGAA	GTTTTTCGATT	CTGATTCGTT	TACCTGGAAG	AGATTAGAAA
ATACACGCTT	CAAAAGCTAA	GACTAAGCAA	ATGGACCTTC	TCTAATCTTT
310	320	330	340	350
*	*	*	*	*
TTTGCGTCTA	CCAAAAACAG	ACAGATTAAT	TTTTTCCAAC	CCGATACAAG
AAACGCAGAT	GGTTTTTGTC	TGTCTAATTA	AAAAAGGTTG	GGCTATGTTC
360	370	380	390	400
*	*	*	*	*
TTTCGGGGTT	CTTGCAATTGG	ATATCACGGA	ACAACAATGT	GATCCGGTTT
AAAGCCCCAA	GAACGTAACC	TATAGTGGCT	TGTTGTTACA	CTAGGCCAAA
410	420	430	440	450
*	*	*	*	*
TGTCTCAAAA	CCGAAACTTG	GTCCTTCTTC	CATACTCCGA	ACTCTGATGT
ACAGAGTTTT	GGCTTTGAAC	CAGGAAGAAG	GTATGAGGCT	TGAGACTACA
460	470	480	490	500
*	*	*	*	*
TTTCTCAGGA	TTAGTCAGAT	ACGAAGGGAA	GCTAGGTGCT	ATTCTGTCAGT
AAAGAGTCCT	AATCAGTCTA	TGCTTCCCTT	CGATCCACGA	TAAGCAGTCA
510	520	530	540	550
*	*	*	*	*
GGACAAACAA	AGATCAAGAA	GATGTTTCAG	AGTTATGGGT	TTTAAAGAGC

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Fig. 4

CCTGTTTGTT TCTAGTTCTT CTACAAGTGC TCAATACCCA AAATTTCTCG  
 560 570 580 590 600  
 \* \* \* \* \*  
 AGTTTTGAAA AGTCGTGGGT TAAAGTGAAA GATATTAAAA GCATTGGAGT  
 TCAAAACTTT TCAGCACCCA ATTTCACTTT CTATAATTTT CGTAACCTCA  
 610 620 630 640 650  
 \* \* \* \* \*  
 AGATTTGATT ACGTGGACTC CAAGCAACGA CGTTGTATTG TTTTCGTAGTA  
 TCTAAACTAA TGCACCTGAG GTTCGTTGCT GCAACATAAC AAAGCATCAT  
 660 670 680 690 700  
 \* \* \* \* \*  
 GTGATCGTGG TTGCCTCTAC AACATAAACG CAGAGAAGTT GAATTTAGTT  
 CACTAGCACC AACGGAGATG TTGTATTTGC GTCTCTTCAA CTTAAATCAA  
 710 720 730 740 750  
 \* \* \* \* \*  
 TATGCAAAAA AAGAGGGATC TGATTGTTCT TTCGTTTGTT TTCCGTTTTG  
 ATACGTTTTT TTCTCCCTAG ACTAACAAGA AAGCAAACAA AAGGCAAAAC  
 760 770 780 790 800  
 \* \* \* \* \*  
 TTCTGATTAC GAGAGGGTTG ATCTGAACGG AAGAAGCAAC GGGCCGACAC  
 AAGACTAATG CTCTCCCAAC TAGACTTGCC TTCTTCGTTG CCCGGCTGTG  
 810 820 830 840 850  
 \* \* \* \* \*  
 TTTAAAAAAA AAATAAAAAA AATGGGCCGA CAAATGCAAA CGTAGTTGAC  
 AAATTTTTTT TTTATTTTTT TTACCCGGCT GTTTACGTTT GCATCAACTG  
 860 870 880 890 900  
 \* \* \* \* \*  
 AAGGATCTCA AGTCTCAAGT CTCAATTGGC TCGCTCATTG TGGGGCATAA  
 TTCCTAGAGT TCAGAGTTCA GAGTTAACCG AGCGAGTAAC ACCCCGTATT  
 910 920 930 940 950  
 \* \* \* \* \*  
 ATATATCTAG TGATGTTTAA TTGTTTTTTA TAAGGTAAAA AGGAATATTG  
 TATATAGATC ACTACAAATT AACAAAAAAT ATTCCATTTT TCCTTATAAC  
 960 970 980 990 1000  
 \* \* \* \* \*  
 AATTTTGTTT CTTAGGTTTA TGTAATAATA CCAAACATTG TTTTATGAAT  
 TTA AACAAA GAATCCAAAT ACATTATTAT GGTTTGTAAC AAAATACTTA  
 1010 1020 1030 1040 1050  
 \* \* \* \* \*  
 ATTTAATCTG ATTTTTTGGC TAGTTATTTT ATTATATCAA GGGTTCCTGT  
 TAAATTAGAC TAAAAAACCG ATCAATAAAA TAATATAGTT CCCAAGGACA  
 1060 1070 1080 1090 1100  
 \* \* \* \* \*



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Fig. 4

TTATAGTTGA	AAACAGTTAC	TGTATAGAAA	ATAGTGTCCC	AATTTTCTCT
AATATCAACT	TTTGTCAATG	ACATATCTTT	TATCACAGGG	TTAAAAGAGA
1110	1120	1130	1140	1150
*	*	*	*	*
CTTAAATAAT	ATATTAGTTA	ATAAAAAGATA	TTTTAATATA	TTAGATATAC
GAATTTATTA	TATAATCAAT	TATTTTCTAT	AAAATTATAT	AATCTATATG
1160	1170	1180	1190	1200
*	*	*	*	*
AATAATATCT	AAAGCAACAC	ATATTTAGAC	ACAACACGTA	ATATCTTACT
TTATTATAGA	TTTCGTTGTG	TATAAATCTG	TGTTGTGCAT	TATAGAATGA
1210	1220	1230	1240	1250
*	*	*	*	*
ATTGTTTACA	TATATTTATA	GCTTACCAAT	ATAACCCGTA	TCTATGTTTT
TAACAAATGT	ATATAAATAT	CGAATGGTTA	TATTGGGCAT	AGATACAAAA
1260	1270	1280	1290	1300
*	*	*	*	*
ATAAGCTTTT	ATACAATATA	TGTACGGTAT	GCTGTCCACG	TATATATATT
TATTCGAAAA	TATGTTATAT	ACATGCCATA	CGACAGGTGC	ATATATATAA
1310	1320	1330	1340	1350
*	*	*	*	*
CTCCAAAAAA	AACGCATGGT	ACACAAAATT	TATTAAATAT	TTGGCAATTG
GAGGTTTTTT	TTGCGTACCA	TGTGTTTTAA	ATAATTTATA	AACCGTTAAC
1360	1370	1380	1390	1400
*	*	*	*	*
GGTGTTTATC	TAAAGTTTAT	CACAATATTT	ATCAACTATA	ATAGATGGTA
CCACAAATAG	ATTTCAAATA	GTGTTATAAA	TAGTTGATAT	TATCTACCAT
1410	1420	1430	1440	1450
*	*	*	*	*
GAAGATAAAA	AAATTATATC	AGATTGATTC	AATTAAATTT	TATAATATAT
CTTCTATTTT	TTTAATATAG	TCTAACTAAG	TTAATTTAAA	ATATTATATA
1460	1470	1480	1490	1500
*	*	*	*	*
CATTTTAAAA	AATTAATTAA	AAGAAAACCTA	TTTCATAAAA	TTGTTCAAAA
GTAAAATTTT	TTAATTAATT	TTCTTTTGAT	AAAGTATTTT	AACAAGTTTT
1510	1520	1530	1540	1550
*	*	*	*	*
GATAATTAGT	AAAATTAATT	AAATATGTGA	TGCTATTGAA	TTATAGAGAG
CTATTAATCA	TTTTAATTAA	TTTATACACT	ACGATAACTT	AATATCTCTC
1560	1570	1580	1590	1600
*	*	*	*	*
TTATTGTAAA	TTTACTTAAA	ATCATACAAA	TCTTATCCTA	ATTTAACTTA
AATAACATTT	AAATGAATTT	TAGTATGTTT	AGAATAGGAT	TAAATTGAAT
1610	1620	1630	1640	1650

Fig. 4

TCATTTAAGA	AATACAAAAG	TAAAAAACGC	GGAAAGCAAT	AATTTATTTA
AGTAAATTCT	TTATGTTTTT	ATTTTTTGCG	CCTTTCGTTA	TTAAATAAAAT
1660	1670	1680	1690	1700
CCTTATTATA	ACTCCTATAT	AAAGTACTCT	GTTTATTCAA	CATAATCTTA
GGAATAATAT	TGAGGATATA	TTTCATGAGA	CAAATAAGTT	GTATTAGAAT
1710	1720	1730	1740	1750
CGTTGTTGTA	TTCATAGGCA	TCTTTAACCT	ATCTTTTCAT	TTTCTGATCT
GCAACAACAT	AAGTATCCGT	AGAAATTGGA	TAGAAAAGTA	AAAGACTAGA
1760	1770	1780	1790	1800
CGATCGTTTT	CGATCCAACA	AAATGAGTCT	ACCGGTGAGG	AACCAAGAGG
GCTAGCAAAA	GCTAGGTTGT	TTTACTCAGA	TGGCCACTCC	TTGGTTCTCC
1810	1820	1830	1840	1850
TGATTATGCA	GATTCCTTCT	TCTTCTCAGT	TTCCAGCAAC	ATCGAGTCCG
ACTAATACGT	CTAAGGAAGA	AGAAGAGTCA	AAGGTCGTTG	TAGCTCAGGC
1860	1870	1880	1890	1900
GAAAACACCA	ATCAAGTGAA	GGATGAGCCA	AATTTGTTTA	GACGTGTTAT
CTTTTGTGGT	TAGTTCACCT	CCTACTCGGT	TTAAACAAAT	CTGCACAATA
1910	1920	1930	1940	1950
GAATTTGCTT	TTACGTCGTA	GTTATTGAAA	AAGCTGATTT	ATCGCATGAT
CTTAAACGAA	AATGCAGCAT	CAATAACTTT	TTCGACTAAA	TAGCGTACTA
1960	1970	1980	1990	2000
TCAGAACGAG	AAGTTGAAGG	CAAATAACTA	AAGAAGTCTT	TTATATGTAT
AGTCTTGCTC	TTCAACTTCC	GTTTATTGAT	TTCTTCAGAA	AATATACATA
2010	2020	2030	2040	2050
ACAATAATTG	TTTTTAAATC	AAATCCTAAT	TAAAAAATA	TATTCATTAT
TGTTATTAAC	AAAAATTTAG	TTTAGGATTA	ATTTTTTTAT	ATAAGTAATA
2060	2070	2080	2090	2100
GACTTTCATG	TTTTTAATGT	AATTTATTCC	TATATCTATA	ATGATTTTTG
CTGAAAGTAC	AAAAATTACA	TTAAATAAGG	ATATAGATAT	TACTAAAAAC
2110	2120	2130	2140	2150
TTGTGAAGAG	CGTTTTTATT	TGCTATAGAA	CAAGGAGAAT	AGTTCCAGGA
AACACTTCTC	GCAAAAAGTAA	ACGATATCTT	GTTCTCTTA	TCAAGGTCCT

Fig. 4

2160	2170	2180	2190	2200
*	*	*	*	*
AATATTCGAC	TTGATTTAAT	TATAGTGTAA	ACATGCTGAA	CACTGAAAAT
TTATAAGCTG	AACTAAATTA	ATATCACATT	TGTACGACTT	GTGACTTTTA
2210	2220	2230	2240	2250
*	*	*	*	*
TACTTTTTTCA	ATAAACGAAA	AATATAATAT	ACATTACAAA	ACTTATGTGA
ATGAAAAAGT	TATTTGCTTT	TTATATTATA	TGTAATGTTT	TGAATACACT
2260	2270	2280	2290	2300
*	*	*	*	*
ATAAAGCATG	AGACTTAATA	TACGTTCCCT	TTATCATTTT	ACTTCAAAGA
TATTTTCGTAC	TCTGAATTAT	ATGCAAGGGA	AATAGTAAAA	TGAAGTTTCT
2310	2320	2330	2340	2350
*	*	*	*	*
AAATAAACAG	AAATGTAAC	TTCACATGTA	AATCTAATTC	TTAAATTTAA
TTTATTTGTC	TTTACATTGA	AAGTGTACAT	TTAGATTAAG	AATTTAAATT
2360	2370	2380	2390	2400
*	*	*	*	*
AAAATAATAT	TTATATATTT	ATATGAAAAT	AACGAACCGG	ATGAAAAATA
TTTTATTATA	AATATATAAA	TATACTTTTA	TTGCTTGGCC	TACTTTTTAT
2410	2420	2430	2440	2450
*	*	*	*	*
AATTTTATAT	ATTTATATCA	TCTCCAAATC	TAGTTTGGTT	CAGGGGCTTA
TTAAAATATA	TAAATATAGT	AGAGGTTTAG	ATCAAACCAA	GTCCCCGAAT
2460	2470	2480	2490	2500
*	*	*	*	*
CCGAACCGGA	TTGAACTTCT	CATATACAAA	AATTAGCAAC	ACAAAATGTC
GGCTTGGCCT	AACTTGAAGA	GTATATGTTT	TTAATCGTTG	TGTTTTACAG
2510	2520	2530	2540	2550
*	*	*	*	*
TCCGGTATAA	ATACTAACAT	TTATAACCCG	AACCGGTTTA	GCTTCCTGTT
AGGCCATATT	TATGATTGTA	AATATTGGGC	TTGGCCAAAT	CGAAGGACAA
2560	2570	2580	2590	2600
*	*	*	*	*
ATATCTTTTT	AAAAAAGATC	TCTGACAAAG	ATTCCTTTCC	TGGAAATTTA
TATAGAAAAA	TTTTTTCTAG	AGACTGTTTC	TAAGGAAAGG	ACCTTTAAAT
2610	2620	2630	2640	2650
*	*	*	*	*
CCGGTTTTTG	TGAAATGTAA	ACCGTGGGAC	GAGGATGCTT	CTTCATATCT
GGCCAAAACC	ACTTTACATT	TGGCACCTTG	CTCCTACGAA	GAAGTATAGA
2660	2670	2680	2690	2700
*	*	*	*	*
CACCACCACT	CTCGTTGACT	GGACTTGGCT	CTGCTCGTCA	ATGGTTATCT
GTGGTGGTGA	GAGCAACTGA	CCTGAACCGA	GACGAGCAGT	TACCAATAGA

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Fig. 4

2710	2720	2730	2740	2750
*	*	*	*	*
TCGATCTTAA	ACCAAATCCA	GTTGATAAGG	TCTCTTCGTT	GATTAGCAGA
AGCTAGAATT	TGGTTTAGGT	CAACTATTCC	AGAGAAGCAA	CTAATCGTCT
2760	2770	2780	2790	2800
*	*	*	*	*
GATCTCTTTA	ATTTGTGAAT	TTCAATTCAT	CGGAACCTGT	TGATGGACAC
CTAGAGAAAT	TAAACACTTA	AAGTTAAGTA	GCCTTGGACA	ACTACCTGTG
2810	2820	2830	2840	2850
*	*	*	*	*
CACCATTGAT	GGATTGCGCG	ATTCTTATGA	AATCAGCAGC	ACTAGTTTCG
GTGGTAACTA	CCTAAGCGGC	TAAGAATACT	TTAGTCGTCG	TGATCAAAGC
2860	2870	2880	2890	2900
*	*	*	*	*
TCGCTACCGA	TAACACCGAC	TCCTCTATTG	TTTATCTGGC	CGCCGAACAA
AGCGATGGCT	ATTGTGGCTG	AGGAGATAAC	AAATAGACCG	GCGGCTTGTT
2910	2920	2930	2940	2950
*	*	*	*	*
GTACTCACCG	GACCTGATGT	ATCTGCTCTG	CAATTGCTCT	CCAACAGCTT
CATGAGTGGC	CTGGACTACA	TAGACGAGAC	GTTAACGAGA	GGTTGTCGAA
2960	2970	2980	2990	3000
*	*	*	*	*
CGAATCCGTC	TTTGACTCGC	CGGATGATTT	CTACAGCGAC	GCTAAGCTTG
GCTTAGGCAG	AAACTGAGCG	GCCTACTAAA	GATGTCGCTG	CGATTCGAAC
3010	3020	3030	3040	3050
*	*	*	*	*
TTCTCTCCGA	CGGCCGGGAA	GTTTCTTTCC	ACCGGTGCGT	TTTGTGAGCG
AAGAGAGGCT	GCCGGCCCTT	CAAAGAAAGG	TGGCCACGCA	AAACAGTCGC
3060	3070	3080	3090	3100
*	*	*	*	*
AGAAGCTCTT	TCTTCAAGAG	CGCTTTAGCC	GCCGCTAAGA	AGGAGAAAGA
TCTTCGAGAA	AGAAGTTCTC	GCGAAATCGG	CGGCGATTCT	TCCTCTTTCT
3110	3120	3130	3140	3150
*	*	*	*	*
CTCCAACAAC	ACCGCCGCCG	TGAAGCTCGA	GCTTAAGGAG	ATTGCCAAGG
GAGGTTGTTG	TGGCGGCGGC	ACTTCGAGCT	CGAATTCCTC	TAACGGTTCC
3160	3170	3180	3190	3200
*	*	*	*	*
ATTACGAAGT	CGGTTTCGAT	TCGGTTGTGA	CTGTTTGGC	TTATGTTTAC
TAATGCTTCA	GCCAAAGCTA	AGCCAACACT	GACAAAACCG	AATACAAATG
3210	3220	3230	3240	3250
*	*	*	*	*
AGCAGCAGAG	TGAGACCGCC	GCCTAAAGGA	GTTTCTGAAT	GCGCAGACGA

Fig. 4

TCGTCGTCTC ACTCTGGCGG CGGATTTTCCT CAAAGACTTA CGCGTCTGCT

3260 3270 3280 3290 3300  
\* \* \* \* \*

GAATTGCTGC CACGTGGCTT GCCGGCCGGC GGTGGATTTC ATGTTGGAGG  
CTTAACGACG GTGCACCGAA CGGCCGGCCG CCACCTAAAG TACAACCTCC

3310 3320 3330 3340 3350  
\* \* \* \* \*

TTCTCTATTT GGCTTTCATC TTCAAGATCC CTGAATTAAT TACTCTCTAT  
AAGAGATAAA CCGAAAGTAG AAGTTCTAGG GACTTAATTA ATGAGAGATA

3360 3370 3380 3390 3400  
\* \* \* \* \*

CAGGTAAAAC ACCATCTGCA TTAAGCTATG GTTACACATT CATGAATATG  
GTCCATTTTG TGGTAGACGT AATTCGATAC CAATGTGTAA GTACTTATAC

3410 3420 3430 3440 3450  
\* \* \* \* \*

TTCTTACTTG AGTACTTGTA TTTGTATTTT AGAGGCACTT ATTGGACGTT  
AAGAATGAAC TCATGAACAT AAACATAAAG TCTCCGTGAA TAACCTGCAA

3460 3470 3480 3490 3500  
\* \* \* \* \*

GTAGACAAAG TTGTTATAGA GGACACATTG GTTATACTCA AGCTTGCTAA  
CATCTGTTTC AACAAATATCT CCTGTGTAAC CAATATGAGT TCGAACGATT

3510 3520 3530 3540 3550  
\* \* \* \* \*

TATATGTGGT AAAGCTTGTA TGAAGCTATT GGATAGATGT AAAGAGATTA  
ATATACACCA TTTCGAACAT ACTTCGATAA CCTATCTACA TTTCTCTAAT

3560 3570 3580 3590 3600  
\* \* \* \* \*

TTGTCAAGTC TAATGTAGAT ATGGTTAGTC TTGAAAAGTC ATTGCCGGAA  
AACAGTTCAG ATTACATCTA TACCAATCAG AACTTTTCAG TAACGGCCTT

3610 3620 3630 3640 3650  
\* \* \* \* \*

GAGCTTGTTA AAGAGATAAT TGATAGACGT AAAGAGCTTG GTTTGGAGGT  
CTCGAACAAT TTCTCTATTA ACTATCTGCA TTTCTCGAAC CAAACCTCCA

3660 3670 3680 3690 3700  
\* \* \* \* \*

ACCTAAAGTA AAGAAACATG TCTCGAATGT ACATAAGGCA CTTGACTCGG  
TGGATTTTCAT TTCTTTGTAC AGAGCTTACA TGTATTCCGT GAACTGAGCC

3710 3720 3730 3740 3750  
\* \* \* \* \*

ATGATATTGA GTTAGTCAAG TTGCTTTTGA AAGAGGATCA CACCAATCTA  
TACTATAACT CAATCAGTTC AACGAAAACCT TTCTCCTAGT GTGGTTAGAT

3760 3770 3780 3790 3800  
\* \* \* \* \*

Fig. 4

GATGATGCGT GTGCTCTTCA TTTCGCTGTT GCATATTGCA ATGTGAAGAC  
CTACTACGCA CACGAGAAGT AAAGCGACAA CGTATAACGT TACACTTCTG

3810 3820 3830 3840 3850  
\* \* \* \* \*

CGCAACAGAT CTTTTTAAAC TTGATCTTGC CGATGTCAAC CATAGGAATC  
GCGTTGTCTA GAAAATTTTG AACTAGAACG GCTACAGTTG GTATCCTTAG

3860 3870 3880 3890 3900  
\* \* \* \* \*

CGAGGGGATA TACGGTGCTT CATGTTGCTG CGATGCGGAA GGAGCCACAA  
GCTCCCCTAT ATGCCACGAA GTACAACGAC GCTACGCCTT CCTCGGTGTT

3910 3920 3930 3940 3950  
\* \* \* \* \*

TTGATACTAT CTCTATTGGA AAAAGGTGCA AGTGCATCAG AAGCAACTTT  
AACTATGATA GAGATAACCT TTTTCCACGT TCACGTAGTC TTCGTTGAAA

3960 3970 3980 3990 4000  
\* \* \* \* \*

GGAAGGTAGA ACCGCACTCA TGATCGCAAA ACAAGCCACT ATGGCGGTTG  
CCTTCCATCT TGGCGTGAGT ACTAGCGTTT TGTTCGGTGA TACCGCCAAC

4010 4020 4030 4040 4050  
\* \* \* \* \*

AATGTAATAA TATCCCGGAG CAATGCAAGC ATTCTCTCAA AGGCCGACTA  
TTACATTATT ATAGGGCCTC GTTACGTTTCG TAAGAGAGTT TCCGGCTGAT

4060 4070 4080 4090 4100  
\* \* \* \* \*

TGTGTAGAAA TACTAGAGCA AGAAGACAAA CGAGAACAAA TTCCTAGAGA  
ACACATCTTT ATGATCTCGT TCTTCTGTTT GCTCTTGTTT AAGGATCTCT

4110 4120 4130 4140 4150  
\* \* \* \* \*

TGTTCTCTCC TCTTTTGCAG TGGCGGCCGA TGAATTGAAG ATGACGCTGC  
ACAAGGAGGG AGAAAACGTC ACCGCCGGCT ACTTAACTTC TACTGCGACG

4160 4170 4180 4190 4200  
\* \* \* \* \*

TCGATCTTGA AAATAGAGGT ATCTATCAAG TCTTATTTCT TATATGTTTG  
AGCTAGAACT TTTATCTCCA TAGATAGTTC AGAATAAAGA ATATACAAAC

4210 4220 4230 4240 4250  
\* \* \* \* \*

AATTAAATTT ATGTCCTCTC TATTAGGAAA CTGAGTGAAC TAATGATAAC  
TTAATTTAAA TACAGGAGAG ATAATCCTTT GACTCACTTG ATTACTATTG

4260 4270 4280 4290 4300  
\* \* \* \* \*

TATTCTTTGT GTCGTCCACT GTTTAGTTGC ACTTGCTCAA CGTCTTTTTC  
ATAAGAAACA CAGCAGGTGA CAAATCAACG TGAACGAGTT GCAGAAAAAG

4310 4320 4330 4340 4350

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Fig. 4

\* \* \* \* \*

CAACGGAAGC ACAAGCTGCA ATGGAGATCG CCGAAATGAA GGAACATGT  
GTTGCCTTCG TGTCGACGT TACCTCTAGC GGCTTACTT CCCTTGTACA

4360 4370 4380 4390 4400  
\* \* \* \* \*

GAGTTCATAG TGA CTAGCCT CGAGCCTGAC CGTCTCACTG GTACGAAGAG  
CTCAAGTATC ACTGATCGGA GCTCGGACTG GCAGAGTGAC CATGCTTCTC

4410 4420 4430 4440 4450  
\* \* \* \* \*

AACATCACCG GGTGTAAAGA TAGCACCTTT CAGAATCCTA GAAGAGCATC  
TTGTAGTGGC CCACATTCT ATCGTGGAAT GTCTTAGGAT CTTCTCGTAG

4460 4470 4480 4490 4500  
\* \* \* \* \*

AAAGTAGACT AAAAGCGCTT TCTAAAACCG GTATGGATTC TCACCCACTT  
TTTCATCTGA TTTTCGCGAA AGATTTTGGC CATACCTAAG AGTGGGTGAA

4510 4520 4530 4540 4550  
\* \* \* \* \*

CATCGGACTC CTTATCACAA AAAACAAAAC TAAATGATCT TTAAACATGG  
GTAGCCTGAG GAATAGTGTT TTTTGTTTTG ATTTACTAGA AATTTGTACC

4560 4570 4580 4590 4600  
\* \* \* \* \*

TTTTGTTACT TGCTGTCTGA CCTTGTTTTT TTATCATCAG TGGAACCTCGG  
AAAACAATGA ACGACAGACT GGAACAAAAA AATAGTAGTC ACCTTGAGCC

4610 4620 4630 4640 4650  
\* \* \* \* \*

GAAACGATTC TTCCCGCGCT GTTCGGCAGT GCTCGACCAG ATTATGAACT  
CTTTGCTAAG AAGGGCGCGA CAAGCCGTCA CGAGCTGGTC TAATACTTGA

4660 4670 4680 4690 4700  
\* \* \* \* \*

GTGAGGACTT GACTCAACTG GCTTGCGGAG AAGACGACAC TGCTGAAGAA  
CACTCCTGAA CTGAGTTGAC CGAACGCCTC TTCTGCTGTG ACGACTTCTT

4710 4720 4730 4740 4750  
\* \* \* \* \*

ACGACTACAA AAGAAGCAAA GGTACATGGA AATACAAGAG ACACTAAAGA  
TGCTGATGTT TTCTTCGTTT CCATGTACCT TTATGTTCTC TGTGATTCTT

4760 4770 4780 4790 4800  
\* \* \* \* \*

AGGCCTTTAG TGAGGACAAT TTGGAATTAG GAAATTCGTC CCTGACAGAT  
TCCGGAAATC ACTCCTGTTA AACCTTAATC CTTTAAGCAG GGACTGTCTA

4810 4820 4830 4840 4850  
\* \* \* \* \*

TCGACTTCTT CCACATCGAA ATCAACCGGT GGAAAGAGGT CTAACCGTAA  
AGCTGAAGAA GGTGTAGCTT TAGTTGGCCA CCTTCTCTCA GATTGGCATT

Fig. 4

4860	4870	4880	4890	4900
*	*	*	*	*
ACTCTCTCAT	CGTCGTCGGT	GAGACTCTTG	CCTCTTAGTG	TAATTTTTCG
TGAGAGAGTA	GCAGCAGCCA	CTCTGAGAAC	GGAGAATCAC	ATTAAAAACG
4910	4920	4930	4940	4950
*	*	*	*	*
TGTACCATAT	AATTCTGTTT	TCATGATGAC	TGTAAGTGT	TATGTCTATC
ACATGGTATA	TTAAGACAAA	AGTACTACTG	ACATTGACAA	ATACAGATAG
4960	4970	4980	4990	5000
*	*	*	*	*
GTTGGCGTCA	TATAGTTTCG	CTCTTCGTTT	TGCATCCTGT	GTATTATTGC
CAACCGCAGT	ATATCAAAGC	GAGAAGCAAA	ACGTAGGACA	CATAATAACG
5010	5020	5030	5040	5050
*	*	*	*	*
TGCAGGTGTG	CTTCAAACAA	ATGTTGTAAC	AATTTGAACC	AATGGTATAC
ACGTCCACAC	GAAGTTTGTT	TACAACATTG	TTAAACTTGG	TTACCATATG
5060	5070	5080	5090	5100
*	*	*	*	*
AGATTTGTAA	TATATATTTA	TGTACATCAA	CAATAACCCA	TGATGGTGT
TCTAAACATT	ATATATAAAT	ACATGTAGTT	GTTATTGGGT	ACTACCACAA
5110	5120	5130	5140	5150
*	*	*	*	*
ACAGAGTTGC	TAGAATCAAA	GTGTGAAATA	ATGTCAAATT	GTTTCATCTGT
TGTCTCAACG	ATCTTAGTTT	CACACTTTAT	TACAGTTTAA	CAAGTAGACA
5160	5170	5180	5190	5200
*	*	*	*	*
TGGATATTTT	CCACCAAGAA	CCAAAAGAAT	ATTCAAGTTC	CCTGAACTTC
ACCTATAAAA	GGTGGTTCTT	GGTTTTCTTA	TAAGTTCAAG	GGACTTGAAG
5210	5220	5230	5240	5250
*	*	*	*	*
TGGCAACATT	CATGTTATAT	GTATCTTCCT	AATTCCTTCCT	TTAACCTTTT
ACCGTTGTAA	GTACAATATA	CATAGAAGGA	TTAAGAAGGA	AATTGGAAAA
5260	5270	5280	5290	5300
*	*	*	*	*
GTAAGTCGAA	TTACACAGCA	AGTTAGTTTC	AGGTCTAGAG	ATAAGAGAAC
CATTGAGCTT	AATGTGTCGT	TCAATCAAAG	TCCAGATCTC	TATTCTCTTG
5310	5320	5330	5340	5350
*	*	*	*	*
ACTGAGTGGG	CGTGTAAGGT	GCATTCTCCT	AGTCAGCTCC	ATTGCATCCA
TGACTCACCC	GCACATTCCA	CGTAAGAGGA	TCAGTCGAGG	TAACGTAGGT
5360	5370	5380	5390	5400
*	*	*	*	*
ACATTTGTGA	ATGACACAAG	TTAACAATCC	TTTGCAACAT	TTCTGGGTGC
TGTAAACACT	TACTGTGTTC	AATTGTTAGG	AAACGTGGTA	AAGACCCACG



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Fig. 4

5410	5420	5430	5440	5450
*	*	*	*	*
ATACATGGAA	ACTTCTTCGA	TTGAAACTTC	CCACATGTGC	AGGTGCGTTC
TATGTACCTT	TGAAGAAGCT	AACCTTTGAAG	GGTGTACACG	TCCACGCAAG
5460	5470	5480	5490	5500
*	*	*	*	*
GCTGTCACTG	ATAGACCAAG	AGACTGAAAG	CTTTCACAAA	TTGCCCTCAA
CGACAGTGAC	TATCTGGTTC	TCTGACTTTC	GAAAGTGTTT	AACGGGAGTT
5510	5520	5530	5540	5550
*	*	*	*	*
ATCTTCTGTT	TCTATCGTCA	TGACTCCATA	TCTCCGACCA	CTGGTCATGA
TAGAAGACAA	AGATAGCAGT	ACTGAGGTAT	AGAGGCTGGT	GACCAGTACT
5560	5570	5580	5590	5600
*	*	*	*	*
GCCAGAGCCC	ACTGATTTTG	AGGGAATTGG	GCTAACCATT	TCCGAGCTTC
CGGTCTCGGG	TGACTAAAC	TCCCTTAACC	CGATTGGTAA	AGGCTCGAAG
5610	5620	5630	5640	5650
*	*	*	*	*
TGAGTCCTTC	TTTTTGATGT	CCTTTATGTA	GGAATCAAAT	TCTTCCTTCT
ACTCAGGAAG	AAAAACTACA	GGAAATACAT	CCTTAGTTTA	AGAAGGAAGA
5660	5670	5680	5690	5700
*	*	*	*	*
GACTTGTTGA	TCCAGCCTGC	TTCACAAGGC	TCACCAGGTT	GTAGTCTCCA
CTGAACACCT	AGGTCTGGACG	AAGTGTTCCG	AGTGGTCCAA	CATCAGAGGT
5710	5720	5730	5740	5750
*	*	*	*	*
AAAATATCAT	GGAATTGTAA	GCAAAAACAA	TCCAGACAGA	ACCTGTGATA
TTTTATAGTA	CCTTAACATT	CGTTTTTGTT	AGGTCTGTCT	TGGACACTAT
5760	5770	5780	5790	5800
*	*	*	*	*
GACCCAAGGT	TCTTGCCACA	GTGATCCGGG	TTCGTTAATA	ACAGCAACTA
CTGGGTTCCT	AGAACGGTGT	CACTAGGCCC	AAGCAATTAT	TGTCGTTGAT
5810	5820	5830	5840	5850
*	*	*	*	*
TGTCCGGGTG	AGGACTGGAG	ACGAAGCAAA	CGTCTTTCCT	TTGTGTTACC
ACAGGCCAC	TCCTGACCTC	TGCTTCGTTT	GCAGAAAGGA	AACACAATGG
5860	5870	5880	5890	5900
*	*	*	*	*
TTCTCTCTGA	TATTAGTGAG	AAACCAACGC	CAACTATCAG	TGGACACTTC
AAGAGAGACT	ATAATCACTC	TTTGGTTGCG	GTTGATAGTC	ACCTGTGAAG
5910	5920	5930	5940	5950
*	*	*	*	*
TTTGGTAAGC	GGAAAGCAAG	CGGGAAAAAC	AATCATCAGC	GTCGAGTCCT

Fig. 4

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AAACCATTTCG CCTTTCGTTT GCCCTTTTGT TTAGTAGTCG CAGCTCAGGA
      5960      5970      5980      5990      6000
      *        *        *        *        *
GAGGAAAATC ATCAATTTCA TAGGGGTACT TGCCGTTCAA GTCTTTTGAA
CTCCTTTTAG TAGTTAAAGT ATCCCCATGA ACGGCAAGTT CAGAAAACTT

      6010      6020      6030      6040      6050
      *        *        *        *        *
TCCACTATGA TCAGAGGTCT ACAGTGTGTA AACCCTTCAA TGGACTGTGG
AGGTGATACT AGTCTCCAGA TGTCACAACT TTGGGAAGTT ACCTGACACC

      6060      6070      6080      6090      6100
      *        *        *        *        *
AAACGCCCAA AACGCGCCAC CGAAGGATGC AAATTCAGGA TTAGGGAAAA
TTTGCGGGTT TTGCGCGGTG GCTTCCTACG TTAAAGTCCT AATCCCTTTT

      6110      6120      6130      6140      6150
      *        *        *        *        *
GCTCATATTG CAGTCCACAA GTAGCCCATT AGATGAGTGA AATGCAGCCA
CGAGTATAAC GTCAGGTGTT CATCGGGTAA TCTACTCACT TTACGTCCGT

      6160      6170      6180      6190      6200
      *        *        *        *        *
ATTAGTTTAG GCAATACTCT GAAACTCTGA TCTTTGATTA CTTCTGTTC
TAATCAAATC CGTTATGAGA CTTTGAGACT AGAAACTAAT GAAGGACAAG

      6210      6220      6230      6240      6250
      *        *        *        *        *
TGCTGCCCCG AGCTTTGAAG TTTTAAGCAT GTCACCAAAC TTTTCAACTC
ACGACGGGCG TCGAAACTTC AAAATTCCGT CAGTGGTTTG AAAAGTTGAG

      6260      6270      6280      6290      6300
      *        *        *        *        *
TGCTGTTAGA GTGGGTGTA CCCTGATCAG ACACTCAATC TCTTCTGCTG
ACGACAATCT CACCCAACAT GGGACTAGTC TGTGAGTTAG AGAAGACGAC

      6310      6320      6330      6340      6350
      *        *        *        *        *
CAAATTACAA GTTGAAGTTT TCCGGCTTAA TAGAACAACA AGTATGTGGA
GTTTAATGTT CAACTTCAAA AGGCCGAATT ATCTTGTTGT TCATACACCT

      6360      6370      6380      6390      6400
      *        *        *        *        *
CCAACTACAC TTAGTTATCT TAACAAGTCC ATGTTCTTCT ATTCAATCTG
GGTTGATGTG AATCAATAGA ATTGTTGAGG TACAAGAAGA TAAGTTAGAC

      6410      6420      6430      6440      6450
      *        *        *        *        *
CCCGACGCGA CCAATTGCAT TTCCATCTGA TGCATTTAAA CGTATACTCG
GGGCTGCGCT GGTTAACGTA AAGGTAGACT ACGTAAATTT GCATATGAGC

      6460      6470      6480      6490      6500
      *        *        *        *        *

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TCCTTCTCAA	TCTCTTGTA	TACACACTTT	TGCTGCCCTC	TAATGGAACA
AGGAAGAGTT	AGAGAACATG	ATGTGTGAAA	ACGACGGGAG	ATTACCTTGT
6510	6520	6530	6540	6550
*	*	*	*	*
CCAGTCCACC	GCCTTCTTCA	GCTCATCCCT	ATCTTTAAAA	CACAACCCTA
GGTCAGGTGG	CGGAAGAAGT	CGAGTAGGGA	TAGAAATTTT	GTGTTGGGAT
6560	6570	6580	6590	6600
*	*	*	*	*
CACGCAATTC	ATGATCATCA	ATCCACAAAC	TAGACAAAGT	ACACTGTTTT
GTGCGTTAAG	TACTAGTAGT	TAGGTGTTTG	ATCTGTTTCA	TGTGACAAAA
6610	6620	6630	6640	6650
*	*	*	*	*
GAAGCACTCG	AATCAACAAC	ACCTTTACTT	AATAAGCACG	CATACGGTAA
CTTCGTGAGC	TTAGTTGTTG	TGGAAATGAA	TTATTCGTGC	GTATGCCATT
6660	6670	6680	6690	6700
*	*	*	*	*
TACCTCTAAG	CCTGGCACAT	TCAAACCTTG	TGTGCATCAT	CTGAACCCGA
ATGGAGATTC	GGACCGTGTA	AGTTTGGAAC	ACACGTAGTA	GACTTGGGCT
6710	6720	6730	6740	6750
*	*	*	*	*
GTTTTTATCC	GTTATTTCTC	CATCCCCACC	TCCACGAGTG	CTACCATTTT
CAAAAATAGG	CAATAAAGAG	GTAGGGGTGG	AGGTGCTCAC	GATGGTAAAG
6760	6770	6780	6790	6800
*	*	*	*	*
CGAAGTCAGA	ATTTTCCTCG	TCTTCAATCC	ACCCGTTACT	GTTACCCACT
GCTTCAGTCT	TAAAAGGAGC	AGAAGTTAGG	TGGGCAATGA	CAATGGGTGA
6810	6820	6830	6840	6850
*	*	*	*	*
CCCTGAACCT	CTAAACCATT	ATCTCTCTCT	ACTTTCACAG	ATGCATGTGA
GGGACTTGGA	GATTTGGTAA	TAGAGAGAGA	TGAAAGTGTC	TACGTACACT
6860	6870	6880	6890	6900
*	*	*	*	*
CACATAATCA	GTAGCTTCTT	GGGGTTGTTG	CGTCCTCTGT	GTATTTCGAGG
GTGTATTAGT	CATCGAAGAA	CCCCAACAAC	GCAGGAGACA	CATAAGCTCC
6910	6920	6930	6940	6950
*	*	*	*	*
AACTAGCGGG	ATATTCTATT	ACGGATGAAC	AAGCAGCATG	ATCAGTAACA
TTGATCGCCC	TATAAGATAA	TGCCTACTTG	TTCGTCGTAC	TAGTCATTGT
6960	6970	6980	6990	7000
*	*	*	*	*
TTATCAGATG	TCGATTTTAC	TTCCAAATAC	AACTCCACAT	TTCTTATAGA
AATAGTCTAC	AGCTAAAGTG	AAGGTTTATG	TTGAGGTGTA	AAGAATATCT
7010	7020	7030	7040	7050

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      *           *           *           *           *
AGGATGATAA CTTGGAAGCTT CAAGCATAGT CTCCAAACTA GTGTCGTTCA
TCCTACTATT GAACCTTGAA GTTCGTATCA GAGGTTTGAT CACAGCAAGT

      7060           7070           7080           7090           7100
      *           *           *           *           *
CTACATGAAG AAGTAGATAG ATAAAGAGAT CCGGTGAAAC AACTACAGGA
GATGTACTTC TTCATCTATC TATTTCTCTA GGCCACTTTG TTGATGTCCT

      7110           7120           7130           7140           7150
      *           *           *           *           *
TACTTACCAA AATATATTGA ACACTGATTT CTGCAGCTGC AATCCAAAAA
ATGAATGGTT TTATATAACT TGTGACTAAA GACGTCGACG TTAGGTTTTT

      7160           7170           7180           7190           7200
      *           *           *           *           *
TTGGATAAAG ACCATTCAAC AATGTACTTA ACGCAGTCTT TTGCCTAACC
AACCTATTTT TGGTAAGTTG TTACATGAAT TGCGTCAGAA AACGGATTGG

      7210           7220           7230           7240           7250
      *           *           *           *           *
TTGACCGTTT TAGGAGTGGA TCCTTCATAG TAAACACCAT CAGGACCATA
AACTGGCAAA ATCCTCACCT AGGAAGTATC ATTTGTGGTA GTCCTGGTAT

      7260           7270           7280           7290           7300
      *           *           *           *           *
CTTGGTAGAA CCTTTCTCTC AAGGTTTCCA TCGCCATGAC CATAACAGTC
GAACCATCTT GGAAAGAGAG TTCCAAAGGT AGCGGTACTG GTATTGTCAG

      7310           7320           7330           7340           7350
      *           *           *           *           *
CTGCAGTGAA TTCTAAGAAA AATGTAAAAA ATTTTGGCCT AAATCATAA
GACGTCACCT AAGATTCTTT TTACATTTTT TAAACCGGA TTTGAGTATT

      7360           7370           7380           7390           7400
      *           *           *           *           *
TTCTTAACAT ACGAAACCAT GGAGAACTCC ATGTCTAAAA AATAAAGGCT
AAGAATTGTA TGCTTTGGTA CCTCTTGAGG TACAGATTTT TTATTTCCGA

      7410           7420           7430           7440           7450
      *           *           *           *           *
AAAGCTTTTT GGCACAGAA GCAGATAAAT CCATTCAAAA CACATAAACT
TTTCGAAAAA CCGCTGTCTT CGTCTATTTA GGTAAGTTTT GTGTATTTGA

      7460           7470           7480           7490           7500
      *           *           *           *           *
CTAAACAATA AACAGTGATA CTCAATACTA AGACTTGTAAG AGGTCTACGT
GATTTGTTAT TTGTCACTAT GAGTTATGAT TCTGAACATT TCCAGATGCA

      7510           7520           7530           7540
      *           *           *           *
AACTCAAAAC TGGAGAATTG TCAGATCGGG TGTGGCTAGT AGAAGCTT
TTGAGTTTTG ACCTCTTAAC AGTCTAGCCC ACACCGATCA TCTTCGAA

```

10 20 30 40 50  
\* \* \* \* \*  
TCGATCTTTA ACCAAATCCA GTTGATAAGG TCTCTTCGTT GATTAGCAGA  
AGCTAGAAAT TGGTTTAGGT CAACTATTCC AGAGAAGCAA CTAATCGTCT

60 70 80 90 100  
\* \* \* \* \*  
GATCTCTTTA ATTTGTGAAT TTCAATTCAT CGGAACCTGT TGATGGACAC  
CTAGAGAAAT TAAACACTTA AAGTTAAGTA GCCTTGGACA ACTACCTGTG  
M D T>

110 120 130 140 150  
\* \* \* \* \*  
CACCATTGAT GGATTGCGCCG ATTCTTATGA AATCAGCAGC ACTAGTTTCG  
GTGGTAACCTA CCTAAGCGGC TAAGAATACT TTAGTCGTCTG TGATCAAAGC  
T I D G F A D S Y E I S S T S F>

160 170 180 190 200  
\* \* \* \* \*  
TCGCTACCGA TAACACCGAC TCCTCTATTG TTTATCTGGC CGCCGAACAA  
AGCGATGGCT ATTGTGGCTG AGGAGATAAC AAATAGACCG GCGGCTTGTT  
V A T D N T D S S I V Y L A A E Q>

210 220 230 240 250  
\* \* \* \* \*  
GTACTCACCG GACCTGATGT ATCTGCTCTG CAATTGCTCT CCAACAGCTT  
CATGAGTGGC CTGGACTACA TAGACGAGAC GTTAACGAGA GGTTGTCGAA  
V L T G P D V S A L Q L L S N S F>

260 270 280 290 300  
\* \* \* \* \*  
CGAATCCGTC TTTGACTCGC CGGATGATTT CTACAGCGAC GCTAAGCTTG  
GCTTAGGCAG AAAGTGAAGC GCCTACTAAA GATGTCGCTG CGATTCTGAA  
E S V F D S P D D F Y S D A K L>

310 320 330 340 350  
\* \* \* \* \*  
TTCTCTCCGA CGGCCGGGAA GTTTCTTTCC ACCGGTGCCT TTTGTCAGCG  
AAGAGAGGCT GCCGGCCCTT CAAAGAAAGG TGGCCACGCA AAACAGTCGC  
V L S D G R E V S F H R C V L S A>

360 370 380 390 400  
\* \* \* \* \*  
AGAAGCTCTT TCTTCAAGAG CGCTTTAGCC GCCGCTAAGA AGGAGAAAGA  
TCTTCGAGAA AGAAGTTCTC GCGAAATCGG CGGCGATTCT TCCTCTTTCT  
R S S F F K S A L A A A K K E K D>

410 420 430 440 450  
\* \* \* \* \*  
CTCCAACAAC ACCGCCGCCG TGAAGCTCGA GCTTAAGGAG ATTGCCAAGG  
GAGGTTGTTG TGGCGGCGGC ACTTCGAGCT CGAATTCCTC TAACGGTTCC  
S N N T A A V K L E L K E I A K>

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      460          470          480          490          500
      *            *            *            *            *
ATTACGAAGT CGGTTTCGAT TCGGTTGTGA CTGTTTTGGC TTATGTTTAC
TAATGCTTCA GCCAAAGCTA AGCCAACACT GACAAAACCG AATACAAATG
D Y E V   G F D   S V V   T V L A   Y V Y>

      510          520          530          540          550
      *            *            *            *            *
AGCAGCAGAG TGAGACCGCC GCCTAAAGGA GTTCTGAAT GCGCAGACGA
TCGTCGTCTC ACTCTGGCGG CGGATTTCCT CAAAGACTTA CGCGTCTGCT
S S R   V R P P   P K G   V S E   C A D E>

      560          570          580          590          600
      *            *            *            *            *
GAATTGCTGC CACGTGGCTT GCCGGCCGGC GGTGGATTTT ATGTTGGAGG
CTTAACGACG GTGCACCGAA CGGCCGGCCG CCACCTAAAG TACAACCTCC
N C C   H V A   C R P A   V D F   M L E>

      610          620          630          640          650
      *            *            *            *            *
TTCTCTATTT GGCTTTCATC TTCAAGATCC CTGAATTAAT TACTCTCTAT
AAGAGATAAA CCGAAAGTAG AAGTTCTAGG GACTTAATTA ATGAGAGATA
V L Y L   A F I   F K I   P E L I   T L Y>

      660          670          680          690          700
      *            *            *            *            *
CAGAGGCACT TATTGGACGT TGTAGACAAA GTTGTATATAG AGGACACATT
GTCTCCGTGA ATAACCTGCA ACATCTGTTT CAACAATATC TCCTGTGTAA
Q R H   L L D V   V D K   V V I   E D T L>

      710          720          730          740          750
      *            *            *            *            *
GGTTATACTC AAGCTTGCTA ATATATGTGG TAAAGCTTGT ATGAAGCTAT
CCAATATGAG TTCGAACGAT TATATACACC ATTTCGAACA TACTTCGATA
V I L   K L A   N I C G   K A C   M K L>

      760          770          780          790          800
      *            *            *            *            *
TGGATAGATG TAAAGAGATT ATTGTCAAGT CTAATGTAGA TATGGTTAGT
ACCTATCTAC ATTTCTCTAA TAACAGTTCA GATTACATCT ATACCAATCA
L D R C   K E I   I V K   S N V D   M V S>

      810          820          830          840          850
      *            *            *            *            *
CTTGAAAAGT CATTGCCGGA AGAGCTTGTT AAAGAGATAA TTGATAGACG
GAACTTTTCA GTAACGGCCT TCTCGAACAA TTTCTCTATT AACTATCTGC
L E K   S L P E   E L V   K E I   I D R R>

      860          870          880          890          900
      *            *            *            *            *
TAAAGAGCTT GGTTTGGAGG TACCTAAAGT AAAGAAACAT GTCTCGAATG
ATTTCTCGAA CCAAACCTCC ATGGATTTC A TTTCTTTGTA CAGAGCTTAC
K E L   G L E   V P K V   K K H   V S N>

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Fig. 5

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      910      920      930      940      950
      *        *        *        *        *
TACATAAGGC ACTTGACTCG GATGATATTG AGTTAGTCAA GTTGCTTTTG
ATGTATTCCG TGAAGTGAAG CTACTATAAC TCAATCAGTT CAACGAAAAC
V H K A   L D S   D D I   E L V K   L L L>

      960      970      980      990      1000
      *        *        *        *        *
AAAGAGGATC ACACCAATCT AGATGATGCG TGTGCTCTTC ATTTGCTGTG
TTTCTCCTAG TGTGGTTAGA TCTACTACGC ACACGAGAAG TAAAGCGACA
K E D   H T N L   D D A   C A L   H F A V>

     1010      1020      1030      1040      1050
      *        *        *        *        *
TGCATATTGC AATGTGAAGA CCGCAACAGA TCTTTTAAAA CTTGATCTTG
ACGTATAACG TTACACTTCT GGCGTTGTCT AGAAAAATTTT GAACTAGAAC
A Y C   N V K   T A T D   L L K   L D L>

     1060      1070      1080      1090      1100
      *        *        *        *        *
CCGATGTCAA CCATAGGAAT CCGAGGGGAT ATACGGTGCT TCATGTTGCT
GGCTACAGTT GGTATCCTTA GGCTCCCCTA TATGCCACGA AGTACAACGA
A D V N   H R N   P R G   Y T V L   H V A>

     1110      1120      1130      1140      1150
      *        *        *        *        *
GCGATGCGGA AGGAGCCACA ATTGATACTA TCTCTATTGG AAAAAGGTGC
CGCTACGCCT TCCTCGGTGT TAACATATGAT AGAGATAACC TTTTCCACG
A M R   K E P Q   L I L   S L L   E K G A>

     1160      1170      1180      1190      1200
      *        *        *        *        *
AAGTGCATCA GAAGCAACTT TGGAAGGTAG AACCGCACTC ATGATCGCAA
TTCACGTAGT CTTGTTGAA ACCTTCCATC TTGGCGTGAG TACTAGCGTT
S A S   E A T   L E G R   T A L   M I A>

     1210      1220      1230      1240      1250
      *        *        *        *        *
AACAAGCCAC TATGGCGGTT GAATGTAATA ATATCCCGGA GCAATGCAAG
TTGTTTCGGTG ATACCGCCAA CTTACATTAT TATAGGGCCT CGTTACGTTT
K Q A T   M A V   E C N   N I P E   Q C K>

     1260      1270      1280      1290      1300
      *        *        *        *        *
CATTCTCTCA AAGGCCGACT ATGTGTAGAA ATACTAGAGC AAGAAGACAA
GTAAGAGAGT TTCCGGCTGA TACACATCTT TATGATCTCG TTCTTCTGTT
H S L   K G R L   C V E   I L E   Q E D K>

     1310      1320      1330      1340      1350
      *        *        *        *        *
ACGAGAACAA ATTCCTAGAG ATGTTCTCTC CTCTTTTGCA GTGGCGGCCG
TGCTCTTGTT TAAGGATCTC TACAAGGAGG GAGAAAACGT CACCGCCGGC
R E Q   I P R   D V P P   S F A   V A A>

```

1360 1370 1380 1390 1400  
\* \* \* \* \*  
ATGAATTGAA GATGACGCTG CTCGATCTTG AAAATAGAGT TGCACCTTGCT  
TACTTAACTT CTACTGCGAC GAGCTAGAAC TTTTATCTCA ACGTGAACGA  
D E L K M T L L D L E N R V A L A>

1410 1420 1430 1440 1450  
\* \* \* \* \*  
CAACGTCTTT TTCCAACGGA AGCACAAGCT GCAATGGAGA TCGCCGAAAT  
GTTGCAGAAA AAGGTTGCCT TCGTGTTCGA CGTTACCTCT AGCGGCTTTA  
Q R L F P T E A Q A A M E I A E M>

1460 1470 1480 1490 1500  
\* \* \* \* \*  
GAAGGGAACA TGTGAGTTCA TAGTGACTAG CCTCGAGCCT GACCGTCTCA  
CTTCCCTTGT ACACTCAAGT ATCACTGATC GGAGCTCGGA CTGGCAGAGT  
K G T C E F I V T S L E P D R L>

1510 1520 1530 1540 1550  
\* \* \* \* \*  
CTGGTACGAA GAGAACATCA CCGGTGTAA AGATAGCACC TTTCAGAAATC  
GACCATGCTT CTCTTGTAGT GGCCACATT TCTATCGTGG AAAGTCTTAG  
T G T K R T S P G V K I A P F R I>

1560 1570 1580 1590 1600  
\* \* \* \* \*  
CTAGAAGAGC ATCAAAGTAG ACTAAAAGCG CTTTCTAAAA CCGTGGAAGT  
GATCTTCTCG TAGTTTCATC TGATTTTCGC GAAAGATTTT GGCACCTTGA  
L E E H Q S R L K A L S K T V E L>

1610 1620 1630 1640 1650  
\* \* \* \* \*  
CGGGAAACGA TTCTTCCCGC GCTGTTTCGGC AGTGCTCGAC CAGATTATGA  
GCCCTTTGCT AAGAAGGGCG CGACAAGCCG TCACGAGCTG GTCTAATACT  
G K R F F P R C S A V L D Q I M>

1660 1670 1680 1690 1700  
\* \* \* \* \*  
ACTGTGAGGA CTTGACTCAA CTGGCTTGCG GAGAAGACGA CACTGCTGAG  
TGACACTCCT GAACTGAGTT GACCGAACGC CTCTTCTGCT GTGACGACTC  
N C E D L T Q L A C G E D D T A E>

1710 1720 1730 1740 1750  
\* \* \* \* \*  
AAACGACTAC AAAAGAAGCA AAGGTACATG GAAATACAAG AGACACTAAA  
TTTGCTGATG TTTTCTTCGT TTCCATGTAC CTTTATGTTT TCTGTGATTT  
K R L Q K K Q R Y M E I Q E T L K>

1760 1770 1780 1790 1800  
\* \* \* \* \*  
GAAGGCCTTT AGTGAGGACA ATTTGGAATT AGGAAATTCG TCCCTGACAG  
CTTCCGGAAT TCACTCCTGT TAAACCTTAA TCCTTTAAGC AGGGACTGTC  
K A F S E D N L E L G N S S L T>



1810	1820	1830	1840	1850
*	*	*	*	*
ATTGCACTTC	TTCCACATCG	AAATCAACCG	GTGGAAAGAG	GTCTAACCGT
TAAGCTGAAG	AAGGTGTAGC	TTTAGTTGGC	CACCTTTCTC	CAGATTGGCA
D S T S	S T S	K S T	G G K R	S N R>
1860	1870	1880	1890	1900
*	*	*	*	*
AAACTCTCTC	ATCGTCGTCG	GTGAGACTCT	TGCCTCTTAG	TGTAATTTTT
TTTGAGAGAG	TAGCAGCAGC	CACTCTGAGA	ACGGAGAATC	ACATTAAAAA
K L S	H R R R	*>		
1910	1920	1930	1940	1950
*	*	*	*	*
GCTGTACCAT	ATAATTCTGT	TTTCATGATG	ACTGTAACTG	TTTATGTCTA
CGACATGGTA	TATTAAGACA	AAAGTACTAC	TGACATTGAC	AAATACAGAT
1960	1970	1980	1990	2000
*	*	*	*	*
TCGTTGGCGT	CATATAGTTT	CGCTCTTCGT	TTTGCATCCT	GTGTATTATT
AGCAACCGCA	GTATATCAAA	GCGAGAAGCA	AAACGTAGGA	CACATAATAA
2010	2020	2030	2040	2050
*	*	*	*	*
GCTGCAGGTG	TGCTTCAAAC	AAATGTTGTA	ACAATTTGAA	CCAATGGTAT
CGACGTCCAC	ACGAAGTTTG	TTTACAACAT	TGTTAAACTT	GGTTACCATA
2060	2070	2080	2090	2100
*	*	*	*	*
ACAGATTTGT	AATATATATT	TATGTACATC	AACAATAAAA	AAAAAAAAAA
TGTCTAAACA	TTATATATAA	ATACATGTAG	TTGTTATTTT	TTTTTTTTTT
AAAA				
TTTT				

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FIG. 6A

NPR1 (323) NHRNPRGYTVLHVAAVRKEPQLILSLLEKASASEATLEGR TALNIAKQ (371)  
 N + GYT LH AA + +I LL+ AS +E T+ G TAL IA++  
 ankyrin 3 (740) NAKTKNGYTALHQAQQGHTHIINVLLQNNASPNELTVNGTALAIARR (788)

NPR1 (262) KVKKHVSNVHKALDSDDIELVKLLKED (289)  
 K K +S +H A D + V+LLL+ +  
 ankyrin 3 (313) KTKNGLSPLHMTAQGDHLCVQLLSRN (340)

FIG. 6B

1st repeat (265) KHVSNVHKALDSDDIELVKLLKEDHTNLDAC (297)  
 2nd repeat (294) DDACALHFAVAYCNVKTATDCLKDLADVNHNRN (326)  
 3rd repeat (328) RGYTVLHVAAVRKEPQLILSLLEKASASEATL (360)  
 4th repeat (361) EGR TALMIAKQATMAVECNPIPEQCKHSLKGRL (393)

ANK consensus  
 (Michaely and Bennett) G TPLHLAAR GHVEVVKLLLD GADVNA TK  
 A I SQ NNLDIAEV K NPD D  
 V K T M R Q SI N  
 E

(Bork) t otLHhah tt thht LLt t t

10	20	30	40	50
*	*	*	*	*
GTGACTTTCT	AACTATGGCT	GAAATTGCAG	AACGAAAAAG	ACTTTCCATT
CACTGAAAGA	TTGATACCGA	CTTTAACGTC	TTGCTTTTTTC	TGAAAGGTAA
60	70	80	90	100
*	*	*	*	*
TTTCACTTGA	ATGAAACCCA	AAATGGAAAT	CTATCTCTCT	TCTTCTTCTC
AAAGTGAAC	TACTTTGGGT	TTTACCTTTA	GATAGAGAGA	AGAAGAAGAG
110	120	130	140	150
*	*	*	*	*
TTTTACTACC	TCCATTTCCA	TGGCTTTCCC	TCCTCTACCT	TCCCTAGCTC
AAAATGATGG	AGGTAAAGGT	ACCGAAAGGG	AGGAGATGGA	AGGGATCGAG
160	170	180	190	200
*	*	*	*	*
TTTTCAATTT	CTAGAATATT	CTTTTCTTAG	TCTGTAATTA	TCTATAGCTC
AAAAGTTAAA	GATCTTATAA	GAAAAGAATC	AGACATTAAT	AGATATCGAG
210	220	230	240	250
*	*	*	*	*
AATTTCTAAG	ACAGAACTTA	TGTAAGGCGG	CTTTCTGTAA	TGGATAATAG
TTAAAGATTC	TGTCTTGAAT	ACATTCCGCC	GAAAGACATT	ACCTATTATC
260	270	280	290	300
*	*	*	*	*
TAGGACTGCG	TTTTCTGATT	CGAATGACAT	CAGCGGAAGC	AGTAGTATAT
ATCCTGACGC	AAAAGACTAA	GCTTACTGTA	GTCGCCTTCG	TCATCATATA
310	320	330	340	350
*	*	*	*	*
GCTGCATCGG	CGGCGGCATG	ACTGAATTTT	TCTCGCCGGA	GACTTCGCCG
CGACGTAGCC	GCCGCCGTAC	TGACTTAAAA	AGAGCGGCCT	CTGAAGCGGC
360	370	380	390	400
*	*	*	*	*
GCGGAGATCA	CTTCACTGAA	ACGCCTATCG	GAAACACTGG	AATCTATCTT
CGCCTCTAGT	GAAGTGAATT	TGCGGATAGC	CTTTGTGACC	TTAGATAGAA
410	420	430	440	450
*	*	*	*	*
CGATGCGTCT	TTGCCGGAGT	TTGACTACTT	CGCCGACGCT	AAGCTTGTGG
GCTACGCAGA	AACGGCCTCA	AACTGATGAA	GCGGCTGCGA	TTCGAACACC
460	470	480	490	500
*	*	*	*	*
TTTCCGGCCC	GTGTAAGGAA	ATTCCGGTGC	ACCGGTGCAT	TTTGTGCGCG
AAAGGCCGGG	CACATTCCTT	TAAGGCCACG	TGGCCACGTA	AAACAGCCGC
510	520	530	540	550
*	*	*	*	*
AGGAGTCCGT	TCTTTAAGAA	TTTGTTCCTG	GCTAAAAAGG	AGAAGAATAG
TCCTCAGGCA	AGAAATTCTT	AAACAAGACG	CCATTTTTC	TCTTCTTATC

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560	570	580	590	600
*	*	*	*	*
TAGTAAGGTG	GAATTGAAGG	AGGTGATGAA	AGAGCATGAG	GTGAGCTATG
ATCATTCCAC	CTTAACCTCC	TCCACTACTT	TCTCGTACTC	CACTCGATAC
610	620	630	640	650
*	*	*	*	*
ATGCTGTAAT	GAGTGTATTG	GCTTATTTGT	ATAGTGGTAA	AGTTAGGCCT
TACGACATTA	CTCACATAAC	CGAATAAACA	TATCACCATT	TCAATCCGGA
660	670	680	690	700
*	*	*	*	*
TCACCTAAAG	ATGTGTGTGT	TTGTGTGGAC	AATGACTGCT	CTCATGTGGC
AGTGGATTTC	TACACACACA	AACACACCTG	TTACTGACGA	GAGTACACCG
710	720	730	740	750
*	*	*	*	*
TTGTAGGCCA	GCTGTGGCAT	TCCTGGTTGA	GGTTTTGTAC	ACATCATTTA
AACATCCGGT	CGACACCGTA	AGGACCAACT	CCAAAACATG	TGTAGTAAAT
760	770	780	790	800
*	*	*	*	*
CCTTTCAGAT	CTCTGAATTG	GTTGACAAGT	TTCAGAGACA	CCTACTGGAT
GGAAAGTCTA	GAGACTTAAC	CAACTGTTCA	AAGTCTCTGT	GGATGACCTA
810	820	830	840	850
*	*	*	*	*
ATTCTTGACA	AAACTGCAGC	AGACGATGTA	ATGATGGTTT	TATCTGTTGC
TAAGAACTGT	TTTGACGTCG	TCTGCTACAT	TACTACCAA	ATAGACAACG
860	870	880	890	900
*	*	*	*	*
AAACATTTGT	GGTAAAGCAT	GCGAGAGATT	GCTTTCAAGC	TGCATTGAGA
TTTGTAACA	CCATTTGTA	CGCTCTCTAA	CGAAAGTTCTG	ACGTAACTCT
910	920	930	940	950
*	*	*	*	*
TTATTGTCAA	GTCTAATGTT	GATATCATAA	CCCTTGATAA	AGCCTTGCCT
AATAACAGTT	CAGATTACAA	CTATAGTATT	GGGAACCTATT	TCGGAACGGA
960	970	980	990	1000
*	*	*	*	*
CATGACATTG	TAAAACAAAT	TACTGATTCA	CGAGCGGAAC	TTGGTCTACA
GTACTGTAAC	ATTTTGTTTA	ATGACTAAGT	GCTCGCCTTG	AACCAGATGT
1010	1020	1030	1040	1050
*	*	*	*	*
AGGGCCTGAA	AGCAACGGTT	TTCCTGATAA	ACATGTTAAG	AGGATACATA
TCCCGGACTT	TCGTTGCCAA	AAGGACTATT	TGTACAATTC	TCCTATGTAT
1060	1070	1080	1090	1100
*	*	*	*	*
GGGCATTGGA	TTCTGATGAT	GTTGAATTAC	TACAAATGTT	GCTAAGAGAG

CCCGTAACCT AAGACTACTA CAACTTAATG ATGTTTACAA CGATTCTCTC

1110 1120 1130 1140 1150  
\* \* \* \*

GGGCATACTA CCCTAGATGA TGCATATGCT CTCCATTATG CTGTAGCGTA  
CCCGTATGAT GGGATCTACT ACGTATACGA GAGGTAATAC GACATCGCAT

1160 1170 1180 1190 1200  
\* \* \* \*

TTGCGATGCA AAGACTACAG CAGAACTTCT AGATCTTGCA CTTGCTGATA  
AACGCTACGT TTCTGATGTC GTCTTGAAGA TCTAGAACGT GAACGACTAT

1210 1220 1230 1240 1250  
\* \* \* \*

TTAATCATCA AAATTCAAGG GGATACACGG TGCTGCATGT TGCAGCCATG  
AATTAGTAGT TTTAAGTTCC CCTATGTGCC ACGACGTACA ACGTCGGTAC

1260 1270 1280 1290 1300  
\* \* \* \*

AGGAAAGAGC CTAAAATTGT AGTGTCCCTT TTAACCAAAG GAGCTAGACC  
TCCTTTCTCG GATTTTAAAC TCACAGGGAA AATTGGTTTC CTCGATCTGG

1310 1320 1330 1340 1350  
\* \* \* \*

TTCTGATCTG ACATCCGATG GAAGAAAAGC ACTTCAAATC GCCAAGAGGC  
AAGACTAGAC TGTAGGCTAC CTTCTTTTCG TGAAGTTTAG CGGTTCTCCG

1360 1370 1380 1390 1400  
\* \* \* \*

TCACTAGGCT TGTGGATTTC AGTAAGTCTC CGGAGGAAGG AAAATCTGCT  
AGTGATCCGA ACACCTAAAG TCATTCAGAG GCCTCCTTCC TTTTAGACGA

1410 1420 1430 1440 1450  
\* \* \* \*

TCGAATGATC GGTTATGCAT TGAGATTCTG GAGCAAGCAG AAAGAAGAGA  
AGCTTACTAG CCAATACGTA ACTCTAAGAC CTCGTTCGTC TTTCTTCTCT

1460 1470 1480 1490 1500  
\* \* \* \*

CCCTCTGCTA GGAGAAGCTT CTGTATCTCT TGCTATGGCA GGCGATGATT  
GGGAGACGAT CCTCTTCGAA GACATAGAGA ACGATACCGT CCGCTACTAA

1510 1520 1530 1540 1550  
\* \* \* \*

TGCGTATGAA GCTGTTATAC CTTGAAAATA GAGTTGGCCT GGCTAAACTC  
ACGCATACTT CGACAATATG GAACTTTTAT CTCAACCGGA CCGATTTGAG

1560 1570 1580 1590 1600  
\* \* \* \*

CTTTTTCCAA TGGAAGCTAA AGTTGCAATG GACATTGCTC AAGTTGATGG  
GAAAAAGGTT ACCTTCGATT TCAACGTTAC CTGTAACGAG TTCAACTACC

1610 1620 1630 1640 1650  
\* \* \* \*

CACTTCTGAG	TTCCCACTGG	CTAGCATCGG	CAAAAAGATG	GCTAATGCAC
GTGAAGACTC	AAGGGTGACC	GATCGTAGCC	GTTTTTCTAC	CGATTACGTG
1660	1670	1680	1690	1700
*	*	*	*	*
AGAGGACAAC	AGTAGATTTG	AACGAGGCTC	CTTTCAAGAT	AAAAGAGGAG
TCTCCTGTTG	TCATCTAAAC	TTGCTCCGAG	GAAAGTTCTA	TTTTCTCCTC
1710	1720	1730	1740	1750
*	*	*	*	*
CACTTGAATC	GGCTTAGAGC	ACTCTCTAGA	ACTGTAGAAC	TTGGAAAACG
GTGAACCTAG	CCGAATCTCG	TGAGAGATCT	TGACATCTTG	AACCTTTTGC
1760	1770	1780	1790	1800
*	*	*	*	*
CTTCTTTCCA	CGTTGTTCAG	AAGTTCTAAA	TAAGATCATG	GATGCTGATG
GAAGAAAGGT	GCAACAAGTC	TTCAAGATTT	ATTCTAGTAC	CTACGACTAC
1810	1820	1830	1840	1850
*	*	*	*	*
ACTTGTCTGA	GATAGCTTAC	ATGGGGAATG	ATACGGCAGA	AGAGCGTCAA
TGAACAGACT	CTATCGAATG	TACCCCTTAC	TATGCCGTCT	TCTCGCAGTT
1860	1870	1880	1890	1900
*	*	*	*	*
CTGAAGAAGC	AAAGGTACAT	GGAACCTCAA	GAAATTCTGA	CTAAAGCATT
GACTTCTTCG	TTTCCATGTA	CCTTGAAGTT	CTTTAAGACT	GATTTCGTAA
1910	1920	1930	1940	1950
*	*	*	*	*
CACTGAGGAT	AAAGAAGAAT	ATGATAAGAC	TAACAACATC	TCCTCATCTT
GTGACTCCTA	TTTCTTCTTA	TACTATTCTG	ATTGTTGTAG	AGGAGTAGAA
1960	1970	1980	1990	2000
*	*	*	*	*
GTTCTCTTAC	ATCTAAGGGA	GTAGATAAGC	CCAATAAGCT	CCCTTTTAGG
CAAGGAGATG	TAGATTCCCT	CATCTATTCTG	GGTTATTCTGA	GGGAAAATCC
2010	2020	2030	2040	2050
*	*	*	*	*
AAATAGGTAA	TTGTATTAGG	ATATATGAGG	AAGAAGAGGA	TTTTCTTGTA
TTTATCCATT	AACATAATCC	TATATACTCC	TTCTTCTCCT	AAAAGAACAT
2060	2070	2080	2090	2100
*	*	*	*	*
ACATAGCACT	CTTTCCTTTC	ATCATTTGAT	ATGTCAACAT	ACATACAACA
TGTATCGTGA	GAAAGGAAAG	TAGTAAACTA	TACAGTTGTA	TGTATGTTGT
2110	2120	2130	2140	2150
*	*	*	*	*
GCTGTACCAT	AAACTTGTAT	TGTTGCACTT	ACAACTTTGA	AGAACAGAAT
CGACATGGTA	TTTGAACATA	ACAACGTGAA	TGTTGAAACT	TCTTGTCTTA
2160	2170			

\* \*  
TTATTGAAA AAAAAAAAAA AA  
AATAAACTTT TTTTTTTTTT TT

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50  
\* \* \* \* \*  
MDNSRTAFSDSNDISGSSSICCIGGGMTEFFSPETSPAETSLKRLSETL

100  
\* \* \* \* \*  
ESIFDASLPEFDYFADAKLVVSGPCKEIPVHRCILSARSPFFKNLFCGKK

150  
\* \* \* \* \*  
EKNSSKVELKEVMKEHEVSYDAVMSVLAYLYSGKVRPSPKDVCVCVDNDC

200  
\* \* \* \* \*  
SHVACRPAVAFLVEVLYTSFTFQISELVDKFQRHLLDILDKTAADDVMMV

250  
\* \* \* \* \*  
LSVANICGKACERLLSSCIEIIVKSNVDIITLTKALPHDIVKQITDSRAE

300  
\* \* \* \* \*  
LGLQGPESENGFPDKHVKRIHRALDSDDVELLQMLLREGHTTLDDAYALHY

350  
\* \* \* \* \*  
AVAYCDAKTTAELLDLALADINHQNRSRGYTVLHVAAMRKEPKIVVSLTK

400  
\* \* \* \* \*  
GARPSDLTSDGRKALQIAKRLTRLVDFSKSPEEGKSASNDRLCIEILEQA

450  
\* \* \* \* \*  
ERRDPLLGEASVSLAMAGDDLRLMKLLYLENRVGLAKLLFPMEAKVAMDIA

500  
\* \* \* \* \*  
QVDGTSEFPLASIGKKMANAQRTTVDLNEAPFKIKEEHLNRLRALSRTVE

550  
\* \* \* \* \*  
LGKRFFPRCSEVLNKIMDADDLSEIAYMGNDTAEERQLKKQRYMELQEIL

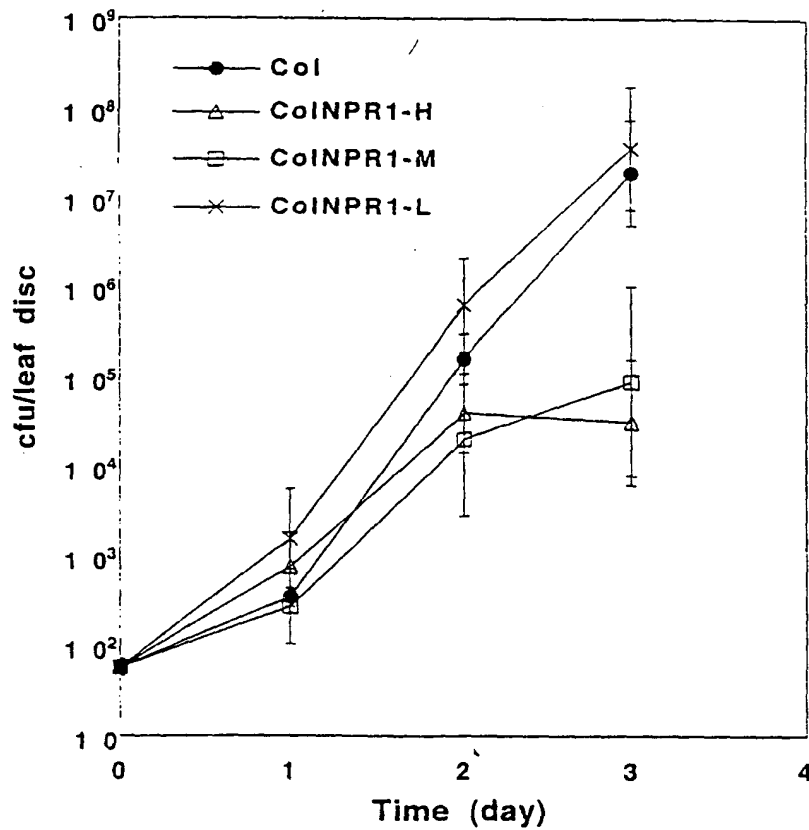
\* \* \* \* \*  
TKAFTEDKEEYDKTNNISSSCSSTSKGVDPKNKLPFRK



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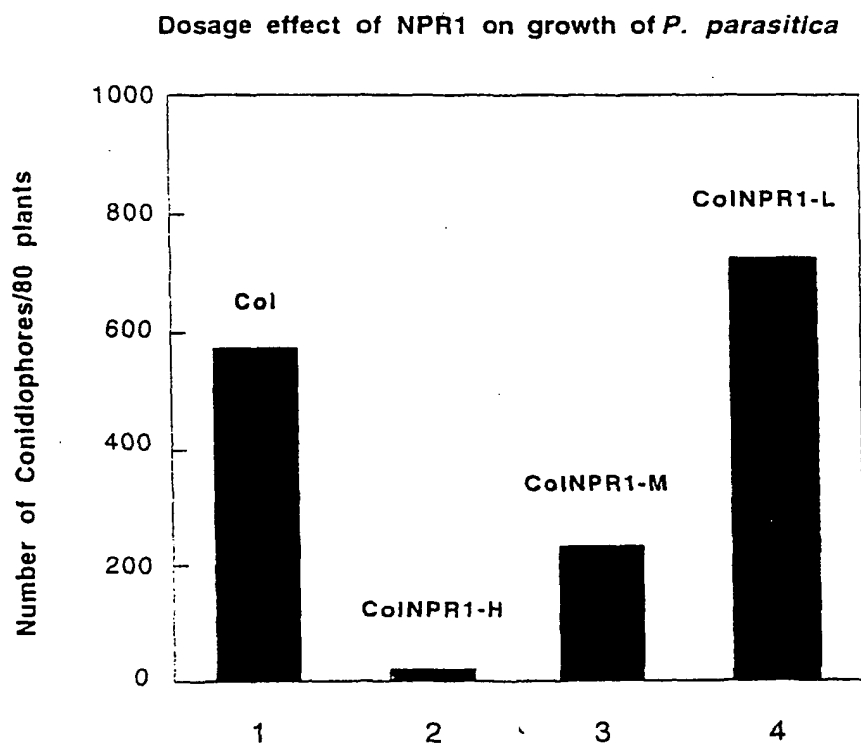
FIG. 8A

Dosage effect of NPR1 on Psm ES4326 resistance



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FIG. 8B



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FIG. 9A

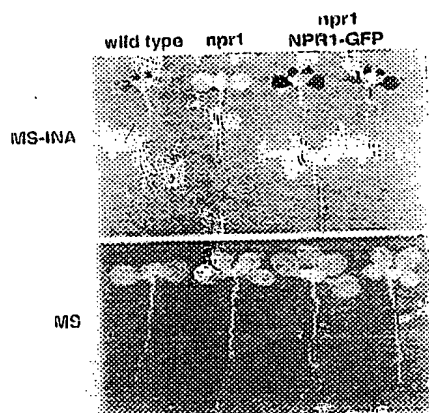


FIG. 9B

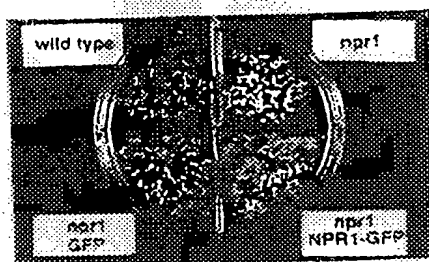
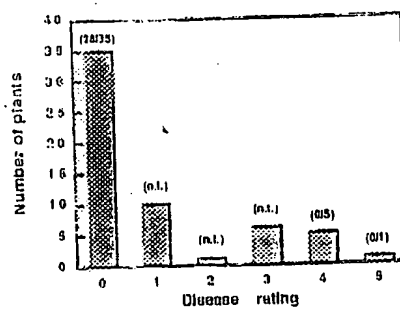
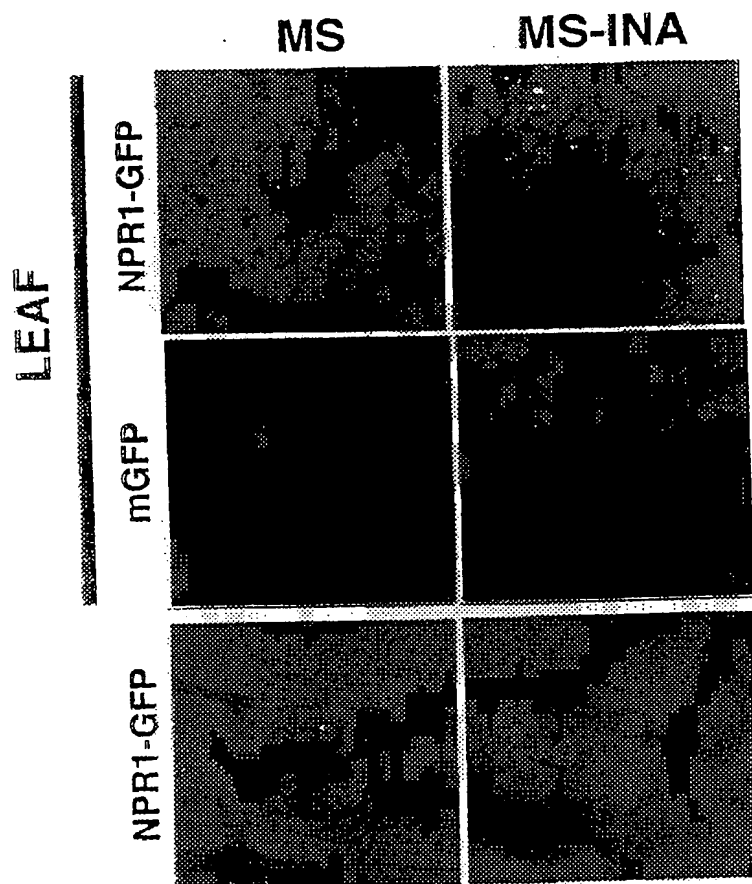


FIG. 9C



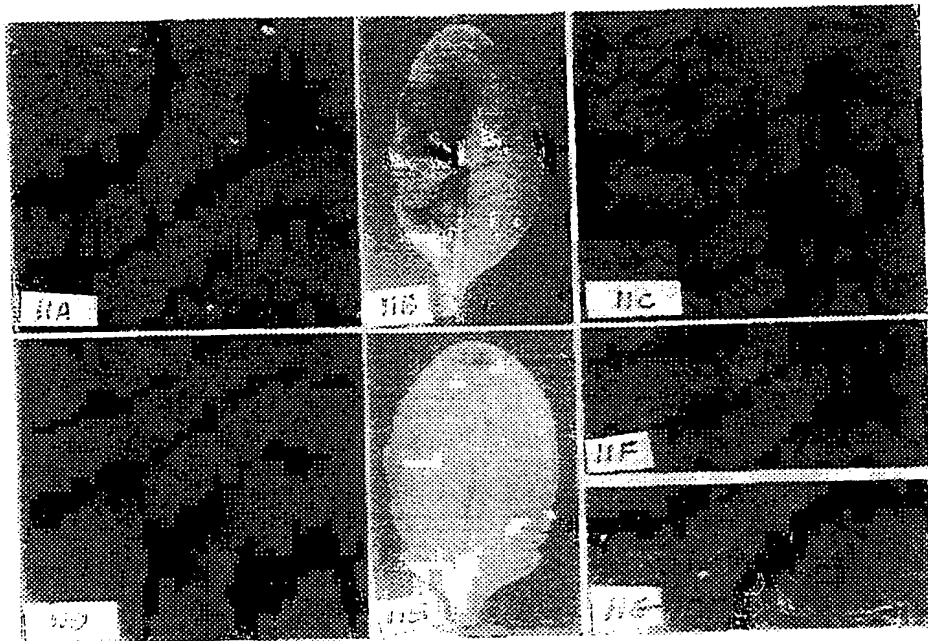
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FIG. 10



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FIGS. 11A-11G



## INTERNATIONAL SEARCH REPORT

International application No.

PCT/US97/13994

**A. CLASSIFICATION OF SUBJECT MATTER**

IPC(6) : C07K 14/00; C07H 21/04; A01H 1/00; C12N 5/00, 15/00

US CL : 435/410; 530/350; 536/23.2; 800/205

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)

U.S. :

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, DIALOG

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	CAO et al. Characterization of an Arabidopsis Mutant That is Nonresponsive to Inducers of Systemic Acquired Resistance. The Plant Cell. November 1994. Vol. 6, pages 1583-1592, see entire article	1-7, 13-25, 31-37
Y	KRASTANOVA et al. Transformation of Grapevine Rootstocks with the Coat Protein Gene of Grapevine Fanleaf Nepovirus. Plant Cell Reports. June 1995. Vol. 14, No. 9, pages 550-554, see entire article.	1-2, 6-7, 13-25, 31-32, 35-36
Y	US 5,304,730 A (LAWSON et al.) 19 April 1994, see entire document.	1-2, 6-7, 13-25, 31-32, 35-36

☒ Further documents are listed in the continuation of Box C.
 ☐ See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
*A* document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
*B* earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
*L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*A* document member of the same patent family
*O* document referring to an oral disclosure, use, exhibition or other means	
*P* document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

16 SEPTEMBER 1997

Date of mailing of the international search report

09 JAN 1998

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## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US97/13994

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	ZHANG et al. Expression of Antisense or Sense RNA of an Ankyrin Repeat Containing Gene Blocks Chloroplast Differentiation in Arabidopsis. The Plant Cell. December 1992, Vol. 4, No. 12, pages 1575-1588.	3

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US97/13994

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
  
2. ☒ Claims Nos.: 8-12, 26-30, 38-41  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:  
  
These claims are directed to SEQ ID NO's. Since no computer-readable form of the disclosed sequences was submitted, these claims could not be searched.
  
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
  
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
  
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
  
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐

The additional search fees were accompanied by the applicant's protest.

☐

No protest accompanied the payment of additional search fees.